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ALIGNMENTS

RESULT 1 Q8SQH5 S 밁 Ş 밁 Ş Query Match Best Local S Matches 291 Yamazaki N., Shinohara Y., Tanida K., Ter "Structural properties of mammalian mitoc identification of possible amino acids th differences in its isoforms.";
Mitochondrion 1:371-379(2002).
EMBL; AB065433; BAB84673.1; -.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3. Q8SQH5; Q8SQH5; 01-JUN-2002 01-JUN-2002 BOS Taurus (Bovine). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. 01-UUN-2002 (TYENBLYE1. 21, Create 01-UUN-2002 (TYENBLYE1. 21, Last s 01-UNR-2003 (TYENBLYE1. 23, Last a 01-UNR-2003 (TYENBLYE1. 23, Last a Adenine nucleotide translocator 2. t Local Simi ches 291; SEQUENCE SEQUENCE FROM N.A. 61 61 1 MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR Similarity GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180 I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120 MTDAAVSFAKDFLAGGVAAAISKTAVAFIERVKLLLQVQHASKQITADKQYKGIIDCVVR 298 AA; Conservative PRELIMINARY; 32955 MW; 97.9%; CARRIER; 3. 5 MW; CB6897BB987B79C0 CRC64; 4. Created)
Last sequence update)
Last annotation update) Pred. No. 5.2e-126; 1; Mismatches 3; Score 1515; DB 6; Length 298; mitochondrial ADP/ATP carriers: that determine B Indels functional <u>,</u> Gaps 60 120 60

Q8BKQ5

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Nat. Genet. 31:135-140(2002).

EMBL; AF506216; AAM34660.1; -

InterPro; IPR001993; Mitoch_carrier.

InterPro; IPR001993; Mitoch_carrier.

InterPro; IPR002007; Mit_uncoupling.

Pfam; PF00153; Mito_carr; 3.

PRINTS; PR00784; MITOCHERIER.

PRINTS; PR00784; MITOCH CARRIER.

PROSITE; PS00215; MITOCH CARRIER; 3.

SEQUENCE 298 AA; 32763 MW; D78663CF65C51D39 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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QI-OCT-2002 (TrEMBLrel. 22, Last sequence to the complex of the co
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Golling G., Amsterdam A., Sun Z., Antonelli M.,
Burgess S., Haldi M., Artzt K., Farrington S.,
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A Milura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

A Milura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

I "The origin and differentiation of the heteromorphic sex

Z, W, X, and Y in the frog Rana rugosa, inferred from the

a sex-linked gene, ADP/ATP translocase.";

Mol. Biol. Evol. 15:1612-1619(1998).

L Mol. Biol. Evol. 15:1612-1619(1998).

I SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMI

R EMBL; AB008463; BAA36513.1; -.

R EMBL; AB008461; BAA36511.1; -.

R EMBL; AB008462; BAA36511.1; -.

R EMBL; AB008462; BAA36512.1; -.

R EMBL; AB008462; BAA36511.1; -.

R EMBL; AB008461; BAA3651.1; -.
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O1-MAY-2000 (TrEMBLrel. 13,
O1-MAR-2003 (TrEMBLrel. 23,
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Amphibia; Batrachia; Anura; Ne
NCBI_TaxID=8410;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
SEQUENCE FROM N.A.
MEDLINE=99083429; PubMed=9866197;
Miura I., Ohtani H., Nakamura M.,
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
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Mol. Biol. Evol. 15:1612-1619(1998).

- - - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

EMBL; AB008469; BAA36510.1; --

EMBL; AB008469; BAA36500.1; --

REMBL; AB008459; BAA36509.1; --

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REMBL; AB008459; BAA36509.1; --

REMBL; AB008459; 
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Q8AYM3;
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"Cold-induced mitochondrial uncoupling and

and ANT mRNA in chicken skeletal muscle.";

FEBS Lett. 0:0-0(2002).

EMBL; AB088686; BAC15533.1; -

SEQUENCE 298 AA; 32847 MW; 1174CC5EC40
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Gallus gallus (Chicken).
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                       Score 1443; DB 13;
Pred. No. 1.2e-119;
9; Mismatches 12;
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Pred. No. 1
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1.2e-119;
ches 10;
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Best Local S
Matches 271
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS001215; MITOCH_CARRIER; 3.
Membrane; Transmembrane; Transport.
SEQUENCE 298 AA; 33068 MW; 158270E
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Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
"The origin and differentiation of the heteromorphic sex chromosomes Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences a sex-linked gene, ADP/ATP translocase.";
Mol. Biol. Evol. 15:1612-1619(1998).
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Rana rugosa (Wrinkled frog).

Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
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01-MAY-1999 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                    QSGRKGTDIMYIGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 297
                                                                                                                                     VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPPDTVRRRMM 240
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QSGRKGABIMYSGTIDCWKKIARDEGSRAFFKGAWSNVLRGMGGAFVLVLYDELKKY
                                                                                                       VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIFISWMIAQSVTAVAGFASYPFDTVRRRMM
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Pred. No. 2.8e-119;
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RESULT 8
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Q919M9;
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01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                              ADP/ATP translocase.
Oryctolagus cuniculus (Rabbit)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Lagomorpha
    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 046373
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus.
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 23, Last annotation updat
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                                                                  Chordata; Craniata; Vei
Lagomorpha; Leporidae;
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Pred. No. 4.9e
11; Mismatches
                                                                                                                                                       Last sequence update)
Last annotation updat
                                                                                                                                                                                                   Created)
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                                                                                       Vertebrata; Euteleostomi;
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RESULT 9
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  Query Match
Best Local Sim
Matches 266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biochem. 335:541-547(1998).

J. Biochem. 335:541-547(1998).

I. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRII

EMBL, AB009386; BAA23777.1; -.

InterPro; IPR001993; Mitoch_carrier.

InterPro; IPR002067; Mit_carrier.

InterPro; IPR002030; Mit_uncoupling.

Pfam; PP00153; Mito carr; 3.

PRINTS; PR00786; MITOCARRIER.

PRINTS; PR00786; MITOCARRIER.

PRINTS; PR00786; MITOCARRIER.

PROSITE; PS00215; MITOCH_CARRIER; 3.

PROSITE; PS00215; MITOCH_CARRIER; 3.

PROSITE; PS00215; MITOCH_CARRIER; 3.
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Q8BVI9;
01-MAR-2003 (TrEMBLrel. 23, C:
01-MAR-2003 (TrEMBLrel. 23, L:
01-MAR-2003 (TrEMBLrel. 23, L:
Solute carrier family 25.
                                                                                                                                                STRAIN-C57BL/6J; TISSUE-Medulla oblongata;
MEDLINE-22354683; PubMed-12466851;
The FANTOM Consortium,
the RIXEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annota
60,770 full-length cDNAs.";
Nature 420.563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamaguchi N., Kasai M.;
Yamaguchi N., Kasai M.;
"Identification of a 30kDa calsequestrin-binding protein, which
"Identification of a 30kDa calsequestrin-binding protein, which
                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                AK078077;
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                                                                                                      298 AA;
91.6%;
ilarity 89.6%;
Conservative 1
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32904 MW;
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89.9%; Pred. No. 7.4e-118;
tive 16; Mismatches 14;
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Last annotation updat
     Score 1417; DI
Pred. No. 2.5e
L5; Mismatches
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Sciurognathi; Muridae;
                                                                                                         F94C89009836710B CRC64;
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                          7; DB 11;
2.5e-117;
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; Murinae; Mus
                                                       298;
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Q91336;
Q91336;
Q91336;
Q1-NOV-1996
                                                                                                                                                                                                                                                                                                        InterPro; IPR001993; Mitoch carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PP00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH CARRIER, 3.
Membrane; Transmembrane; Transport.
SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    Cai Q., Storey K.B.;
Submitted (APR-1999) to t
-i- SIMILARITY: BELONGS T
EMBL; U44832; AAA97882.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97398141; PubMed=9256066; Cai Q., Greenway S.C., Storey K.B.; PubMed=9256066; "Differential regulation of the mitochondrial ADP/ATP in wood frogs under freezing stress."; Biochim. Biophys. Acta 1353:69-78(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rana sylvatica (Wood frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
NCBI_TaxID=45438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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01-MAY-1999 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                              GAAGATSLCFVYPLDFARTRLAADVGKAGABREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                                                   MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIFVSMMIAQSVTAVAGFGSYPFDTVRRRMM
                VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISMMIAQTVTAVAGLTSYPFDTVRRRMM
                                                                                                                                        IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                      I PKEQGF I SFWRGNLANVIRYF PTQALNFGFKDKYKKI FLDNVDKRTQFWRYFAGNLASG
                                                                                                                                                                                  MTDAANSFAKDFLAGGVAAAISKTAVAPIBRVKLLVQVQHASKQITADKQYKGIMDCVVR
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                                                                                                                                                                                                                                                Conservative
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90.1%;
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23,
                                                                                                                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ databases.
TO THE MITOCHONDRIAL CARRIER FAMILY.
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Last
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                                                                                                                                                                                                                                               Score 1295; DB 13;
Pred. No. 1.7e-106;
4; Mismatches 13;
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annotation update)
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RESULT 11
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Best Local Similarity
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Q8IRA0;
01-MAR-2003
01-MAR-2003
01-MAR-2003
CG16944-PC:
                                     Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI TaxID=7227;
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InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH CARRIER; 3.
SEQUENCE 299 AA; 33037 MW; 3C3BBCB26E7C3C5E CRC64;
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
ADP-ATP translocator
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Eukaryota; Metazoa; Ar
     SEQUENCE FROM N.A.
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EMBL; AF401758; AAL02100.
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NCBI_TaxID=62613;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., W., Hockins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Holt R.A., W., Hockins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hockins R.A., Galle R.F.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barlon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Dunkov B.C.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Gosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Howland T.J., Weil M.H., Ibegwam C.,
RA Harris N.L., Howland T.J., Weil M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.B., Kodira C.D., Kraft C., Kraviz S., Kulp D., Lai Z.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Mecheet R.D., Scheeler F., Shen H.,
RA Melson D.R., Nelson K., Saunders R.D., Scheeler F., Shen H.,
RA Melson D.R., Nelson K., Stapleton M., Strong R., Shn B.,
RA Melson D.R., Nelson K., Stapleton M., Strong R., Shn B.,
RA Spier E., Sjradling A.C., Stapleton M., Strong R., Shn B.,
RA Spier E., Sardling A.C., Stapleton M., Strong R., Shn B.,
RA Spier E., Jardling A.C., Stapleton M., Strong R., Shn B.,
RA Spier S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Spier S.M., NoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Jabias R.A., Zhang G., Zhang G., Zhang L., Smith H.O.,
RA Spier S., Scheng L., Shong H., Shith H.O.,
RA Spier S., Shith H.O.,
RA Spier S., Shith H.O.,
RA Spier S.
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A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Corlson K., Dorsett V., Doup L.E., Doyle C., Dreenek D., Farfan D.,
A Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A 'Lbegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
A Stapleton M., Strong R., Svirakas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
"Sequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                       SEQUENCE FROM N.A.
Adams M.D., Celniker S
Submitted (MAR-2000) to
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                                                                                                                                           Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise B., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.";
SEQUENCE FROM N.A
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A., Gocayne J.D.,
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                                                Gibbs R.A., Rubin G.M., Venter C.J., e EMBL/GenBank/DDBJ databases.
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Amanatides P.G., Brandon R.C.,
                                                                                                                                                                                                                                                                                                                       Campbell K., ith C.D.,
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Rogers Y.,
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ID Q9NHW
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AC 01-OC
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Matches 237
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Best Local
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Chen Z., Fair J.A., Batterham P.;
"A cDNA clone encoding the ADP/ATP translocase of Lucilia cuprina.";
submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL; AF218587; AAF32322.1; -.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCHARLER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Membrane; Transmembrane; Transport.
SEQUENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP/ATP translocase.
Lucilla cuprina (Greenbottle fly) (Australian sheep blowfly).
Lucilla cuprina (Greenbottle fly) (Australian sheep blowfly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
Calliphoridae; Lucilia.
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01-OCT-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9NHW5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase;
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TSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGII 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
S mal seek
                                                                                                                   EVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGA
                                                                                                                                                                                                                  LSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVOHASKQITADKQYKGIIDCVVRIPKEQ
                                                                                  GFASYWRGNMANVIRYFPTQALNFAFKDKYKQVFI
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                                                                                                                                                                                          LGFVKDFAAGGISAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMIDCFVRIPKEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRWMMQSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATSLCFVYPLDFARTRLAADTGK-GGQREFTGLGNCLTKIFKSDGIVGLYRGFGVSVQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGFSSFWRGNLANVIRYFPTOALNFAFKDKYKQVFLGGVDKNTQFWRYFAGNLASGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAG
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llarity 81.2%;
Conservative 2
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                                                                                                                                                                                                                                                                                                                                                80.7%;
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Pred. No. 8.1e
21; Mismatches
                                                                                                                                                                                                                                                                                                                           Score 1248.5; DB 5
Pred. No. 2.1e-102;
                                                                                                                                                                                                                                                                                                  Mismatches
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8.1e-103;
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RESULT 15
044094
ID 04409
AC 04409
DT 01-JU
DT 01-JU
DT 01-MA
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AC 04409
AC 04409
AC 01-U
DT 01-U
DT 01-M
DE ADP/B
GN SESB.
OS Dross
OC Eukar
OC Neopt
OC Ephyd
OC APHyd
CO NCBI-
RN [1]
RP SEQUII
RP SEQUII
RP SEQUII
RP SEQUII
RP FLYBB
DR Inter
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DR Inter
DR PINTER
DR PRINTI
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Best Local S
Matches 229
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044093;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 044094;
044094;
01-JUN-1998
01-JUN-1998
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila pseudoobscura (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001993; Mitcoh_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; Mitcotarr; 3.
PRINTS; PR00926; MITCOCARRIER.
PROSITE; PS00215; MITCOCH_CARRIER; 3.
PROSITE; PS00215; Transmembrane; Transport.
Membrane; Repeat; Transmembrane; Transport.
NON TER 288 AA; 31725 MW; 052BOCC00504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER EMBL; AF025798; AAB87883.1; -- FlyBase; FBgn0023392; Dpse\seeB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zeng L.-W., Comeron
Genetica 0:0-0(1997)
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229; Conservative
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                                                                                                                            KATEIIYKNTLHCWATIAKQE-GSAFFKGAFSNVLRGTGGAFVLV
                                                                                                                                                                                                                                          ATSLCFVYPLDFARTRLAADTGK-GGQREFTGLGNCLTKIFKSDGLVGLYRGFGVSVQGI
                                                                                                                                                                                                                                                                                                  QFSSFWRGNLANVIRYFPTQALNFAFKDKYKQVFLGGVDKNTQFWRYFMGNLASGGAAG
                                                                                                                                                                                                                                                                                                                                                         GTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 297
                                                                                                                                               KGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLV
                                                                                                                                                                                  IIYRAAYFGFYDTAR-MLPDPKNTPIYISWAIAQAVTTVAGIVSYPFDTVRRRMMQSGR
                                                                                                                                                                                                  IIYRAAYFGIYDTAKGMLPDPKNTHIVISMMIAQTVTAVAGLTSYPFDTVRRRMMQSGR
                                                                                                                                                                                                                                                          ATSLCFVYFLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGI
                                                                                                                                                                                                                                                                                                                       QEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAG
                                                                                                                                                                                                                                                                                                                                                                                         ALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKE
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 (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comeron J.M., Chen B., Kreitman
                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                             80.4%; =-
20;
                                                                                                                                                                                                                                                                                                                                                                                                                                  77.0%; Score 1190.5; 80.4%; Pred. No. 2.8c
 23,06
Created)
Last sequence update)
Last annotation update)
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                                                         288
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                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length
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Best Local Simi
Matches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila subobscura (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera, Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zeng L.-W., Comeron J.M., Chen B., Kreitman Genetica 0:0-0(1997).
                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                             PROSITE; PS00215; MITOCH_CARRIER; 3.
Membrane; Repeat; Transmembrane; Transport.
NON_TER 288 288
                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002066; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF025799; AAB87884.1; -. FlyBase; FBgm0023237; Dsub\sesB.
                                                                                                                                                                                                                                                                                                                                                                                                                                               - !- SIMILARITY: BELONGS TO THE MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP/ATP translocase (Fragment).
                                                   186
                                                                          185
                                                                                                    127
245
                         245
                                                                                                                              125
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                                                                                                                                                                                                                       5 ALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKB
                                                                                                                                                                                                                                                                         Similarity
KATEIIYKNTIHCWGTIAKQB-GTAFFKGAFSNVLRGTGGAFVLV
                 KGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLV
                                               IIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMQSGR
                                                                                                    ATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGI 184
                                                                                                                                                                       QEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAG
                                                                                                                                                        QGFSSFWRGNLANVIRYFPTQALNFAFKDKYKQVFLGGVDKNTQFWRYFMGNLASGGAAG
                                                                                                                                                                                                         AMGFVKDFAAGGISAAVSKTAVAPIBRVKLLLQVQHISKQISPDKQYKGMVDCFIRIPKE
                                                                                                                                                                                                                                                                                                                288 AA;
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                               31775 MW; 06A1D1E477E81B26 CRC64;
                                                                                                                                                                                                                                                                         76.6%;
80.0%;
                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                         Score 1185.5; DB Pred. No. 7.7e-97
                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                     DB 5;
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Search completed: December 18, 2003, 12:43:10
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Zhou J., Y Margolin J Submitted

SEQUENCE FROM N.A. Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Margolin J.F.;

Bouck J.,

Gibbs R.A.,

(JUL-2000) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.

RC TISSUB-Brain, Cervix, Bye, and Lung;

RX MEDLINE-22388257; PubMedel12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RA Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Butkersley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

MEDLINE-88124845; PubMed-2829183; Houldsworth J., Attardi G.; "Two distinct genes for ADP/ATP translocase are expressed at the mRNA

SEQUENCE OF 36-298 FROM N.A. TISSUE=Liver;

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888	Mamm	Eukaryota; metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;	the	ia;	Chordata; Primates;	ate	85 CE	tar	Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.	rtebra Homini	ta; El dae; I	domo.	3C Om 1			
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RT R	J. P	ADP/ATP translocase."; J. Mol. Biol. 206:261-	18100 1. 20	06:26	translocase."; Biol. 206:261-280(1989)	0 (1	989).									

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EMBL; AY007135; AAG01998.1; -.
EMBL; AY007135; AAG01998.1; -.
EMBL; BC007295; AAH07295.1; -.
EMBL; BC008757; AAH07850.1; -.
REMBL; BC008737; AAH08935.1; -.
RMBL; BC008935; AAH08935.1; -.
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GO; GO:0005744; C:mitochondrial inner membrane translocase
GO; GO:0005471; F:ATP/ADP antiporter activity; NAS.
GO; GO:0006471; P:ATP/ADP exchange; TAS.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR002030; Mitoch_carrier.
InterPro; IPR001993; Mitoch_carrier.
Ifam; PF00153; mito_carr; 3.
PRINTS; PR00784; MITOCARRIER.
PRONTE; P800784; MITOCUPLING.
PROSTE; P800784; MITOCUPLING.
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EMBL; BC014775; AAH14775.1;
PIR; S03894, S03894.
Genew; HGNC:10992; SLC25A6.
MIM; 300151; -.
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Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988)
--- FUNCTION: CATALYZES THE EXCHANGE OF ADP ANI
MITOCHONDRIAL INNER MEMBRANE.
--- SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Multigene family.
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"Two bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues.",
Biochemistry 28:866-873(1989).
-I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
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PIR; B43646; B43646.
InterPro; IPR002057; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Boyidae; Boyinae; Bos.
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01-JUL-1993 (Rel.
16-OCT-2001 (Rel.
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SUBUNIT: Homodimer.
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; pR00784; MITOCH CARRIER.
E; PS00215; MITOCH CARRIER
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.. 26, Last sequence update)
L. 40, Last annotation update
protein, isoform T2 (ADP/ATP
slocator 3) (ANT 3).
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97.7%;
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                                                  Pred. No. 1.9
                                                            Score 1512; DB 1;
Pred. No. 1.9e-125;
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(POTENTIAL)
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(ADP/ATP
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RESULT 3
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MEDLINE=87166056; PubMed=3031073;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraja R.,

Mazzarella R.A., Schlessinger D., Chen B.Y.;

Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                               MEDLINE=88124845;
                                                                                                                                                                                                                                                                                                       SEQUENCE OF 47-298 FROM N.A. TISSUB=Liver;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Becker M., Graves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning of a cDNA for a human growth-regulated.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90375457; PubMed=2168878;
Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga F
"The human fibroblast adenine nucleotide translocator
cloning and sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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            inner membrane.

DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

SIMILARITY: Belongs to the mitochondrial carr
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                                                                                                                                                                                                                                                                                  PubMed=2829183;
                                                                                                                                                                                                                                                                                                                                                                                                 Ozersky P.;
                     to the mitochondrial carrier
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Catarrhini; Hominidae;
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InterPro; IPR002067; Mit carrier.
InterPro; IPR002030; Mit uncoupling.
InterPro; IPR001993; Mitch carrier.
Pfam; PF00153; mito_carr; 3.
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EMBL; J02683; AAA35579.1; --
EMBL; L78810; AAB39266.1; --
EMBL; AC004000; AAB96347.1; --
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PROSITE; PS00215; MITOCH CARRIER;
MITOCHONDRION; Inner membrane; Rep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005887; C:integral to plasma membrane; TAS GO; GO:0015207; F:adenine transporter activity; TAGO; GO:0006832; P:small molecule transport; TAS.
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3 -> L (IN REF. 4 A).
7 -> G (IN REF. 5).
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ADT2 RAT Q09073; 01-FEB-1995

(Rel. 31, Created)

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STRAIN-SD789ue-Dawley; TISSUE-Liver;
MEDLINE-94002161; PubMed-8399300;
Shinohara Y., Kamida M., Yamazaki N., Terada H.;
Shinohara Y., Kamida M., Yamazaki N., Terada H.;
"Isolation and characterization of CDNA clones and a genomic cencoding rat mitochondrial adenine nucleotide translocator.";
Biochim. Biophys. Acta 1152:192-196(1993).
-I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
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                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002067; Mit carrier.
InterPro; IPR002030; Mit carrier.
InterPro; IPR001993; Mitoch carrier.
Pfam; PF00153; mito_carr; 3.
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Mammalia; Eutheria; Rodentia;
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16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, fibroblast isoform (ADP/ATP translocase (Adenine nucleotide translocator 2) (ANT 2).
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Pred. No. 4
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Sciurognathi;
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thi; Muridae; Murinae; Rattus.
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les 9;
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Laplace C.;
Submitted (
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Costet P.,
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p51881; Q61311;
p51881; Q61311;
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last amotation update)
28-FEB-2003 (Rel. 41, Last amotation update)
ADP,ATP carrier protein, fibroblast isoform (in the carrier protein)
                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                 Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=97059403; PubMed=8903724;
Ellison J.W., Li X., Francke U., Shapiro I
"Rapid evolution of human pseudoautosomal
homologs.";
                      EMBL; U27316; AAC52838.1; -.
EMBL; U10404; AAA19009.1; -.
EMBL; X70847; CAA50196.1; -.
EMBL; AF240003; AAF64471.1;
                                                                                                                                                        This
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MEDLINE=20432087; PubMed=10974536;
Levy S.B., Chen Y.-S., Graham B.H.,
"Expression and sequence analysis o
translocase 1 and 2 genes.";
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Mammalia; Eutheria; Rodentia;
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FUNCTION: CATALYZES THE EXCHAMITOCHONDRIAL INNER MEMBRANE.
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                                                                                                                                                                                                         inner membrane
                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
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f the mouse
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Best Local :
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Q0596;
01-FEB-1994 (Rel. 28, C
01-FEB-1994 (Rel. 28, I
16-OCT-2001 (Rel. 40, I
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                                                                                                                                                                            STRAIN-Sprague-Dawley, and Wistar; TIS
MEDLINE-94002161; PubMed-8399300;
Shinohara Y., Kamida M., Yamazaki N.,
"Isolation and characterization of cD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00926; PRINTS; PR00784; MITUNCOUPLING.
PROSITE; PS00215; MITOCH CARRIER; 3.
                                                                                                encoding rat mitochondrial adenine nucleotide translocator.", Biochim. Biophys. Acta 1152:192-196(1993).
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS TH MITOCHONDRIAL INNER MEMBRANE.
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                         SLC25A4 OR ANT1.
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16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle isoform T1
translocase 1) (Adenine nucleotide translocator 1) (ANT 1)
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inner membrane.
TISSUB SPECIFICITY: IN HEART,
EXTENT, IN BRAIN AND KIDNEY.
                                                             SUBCELLULAR LOCATION: Integral
                                                                                    SUBUNIT: Homodimer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
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IPR001993; Mitoch_carrier.
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91.6%;
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5; Mismatches
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                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                     SKELETAL
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                                                             membrane
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                       MUSCLE
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                       AND
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                       A LESSER
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ADT1 MOUSE
ID ADT1 M
AC P49672
AC P49672
DT 01-FEB
DT 15-FEB
DT 15-FEB
DE ADP, AT
DB transl
GN SLC25A
OS Mus mu
OC Mammall
OX NCBI_T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                        ADT1 MOUSE STANDARD; PRT; 298 AA. P48962; Q62164; 01-FEB-1996 (Rel. 33, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) ADP, ATP carrier protein, heart/skeletal muscle i translocase 1) (Adenine nucleotide translocator SIC25A4 OR ANT1 OR ANCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
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TRANSMEM
Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity
267; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                                                                                                                    QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                                                                                                                                                                                                                     VQGIIIYRAAYFGVYDTAKGMLFDPKNTHIVVSWMIAQTVTAVAGVVSYFFDTVRRRMMM 240
                                                                                                                                                                                                                                                                                                                          GAAGATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS
                                                                                                                                                                                                                                                                                                                                                     GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                          IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                   QSGRKGADIMYTGTVDCWRKIAKDEGRKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00215; MITOCH
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298
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                Chordata;
Rodentia;
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brane; Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1424; DB 1;
Pred. No. 1e-117;
                Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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                  Muridae;
                                                                    isoform T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                              Euteleostomi;
                Murinae;
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                                                                     (ADP/ATP) (mANC1).
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in no way
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Darge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Ra Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

C. -i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
                                                                                                                                                                                                 EMBL; U27315; AAC52837.1; -.
EMBL; X74510; CAA52616.1; -.
EMBL; AP2440002; AAF64470.1; -.
EMBL; BC003791; AAH03791.1; -.
EMBL; BC0026925; AAH26925.1; -.
                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Brain;
MEDLINE-97059403; PubMed-8903724;
Ellison J.W., Li X., Francke U., Shapiro L.J.;
"Rapid evolution of human pseudoautosomal genes and their mouse
                       InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch carrier.
Pfam; PF00153; mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
                                                                                                                                                        PIR; S37210; S37210.
MGD; MGI:1353495; S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;

"Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laplace C., Costet P.;
Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mamm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Homodimer.
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    PS00215;
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MITOCH_CARRIER;
                                                                                                                                                          S1c25a4.
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Multigene family
TRANSMEM 12
TRANSMEM 73
TRANSMEM 117
TRANSMEM 117
TRANSMEM 176
TRANSMEM 214
TRANSMEM 273
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P02722;
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CONFLICT
SEQUENCE
                                                                                                                                 MEDLINE-8922903; PubMed=2540808; Powell S.J., Medd S.M., Runswick M.J., "Two bovine genes for mitochondrial ADI differences in various tissues."; Biochemistry 28:866-873(1989).
                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart isoform T1 (ADP/ATP translocase
(Adenine nucleotide translocator 1) (ANT 1).
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REPEAT
                                                                 SEQUENCE MEDILINE=82188267; PubMed=7076130; MEDILINE=82188267; PubMed=7076130; Aquila H., Misra D., Eulitz M., Kling "Complete amino acid sequence of the mitochondria.";
                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                    BOVIN
           MEDLINE=86295775;
Rasmussen U.B., W
                                             Hoppe-Seyler'в
[3]
                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=89229093; Powell S.J., Medd
                                                                                                                                                                                                                                                               Bos taurus (Bovine).
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                                 SEQUENCE
Bovine
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cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs
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                                  OF 207-297
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f the ADP/ATP
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PRINTS; PR00784; MITUNCOUPLING.
PR00215; MITOCH_CARRIER;
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EMBL; M24102; AAA30768.1;
PIR; A43646; XWBO.
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InterPro; IPR002030; Mit_uncoupil
InterPro; IPR001993; Mitoch_carri
Pfam; PP00153; mito_carr; 3
PRINTS; PR00926; MITOCARRIER.
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Res. Commun. 138:850-857(1986)
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Pred. No. 4.1e-117;
9; Mismatches 13;
                     PRT;
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RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Richards S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., WcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RT human and mouse cDNA sequences.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIAINE 8041149; PubMed=2823266;
MEDIAINE-88041149; Made R.P., Shuster R., Wallace D.C.;
Meckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
McDNA sequence of a human skeletal muscle ADP/ATP translocator:
of a leader peptide, divergence from a fibroblast translocator c
and coevolution with mitochondrial DNA genes.";
Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
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Creanshara R.L., Feingold B.A., Grouse L.
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WEDLINE=89340499; PubMed=2547778;

MIDLINE=89340499; PubMed=2547778;

Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,

Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,

Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;

"A human muscle adenine nucleotide translocator gene has four "A human muscle adenine nucleotide translocator gene has four "A human muscle adenine nucleotide translocator gene has four "I blocated on chromosome 4, and is differentially expressed.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89236396; PubMed=2541251;
MEDLINE=89236396; PubMed=2541251;
Malker J.
Malker J.
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01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle i
translocase 1) (Adenine nucleotide translocator
SLC25A4 OR ANT1.
                                                                                                                                                                                                                                                                                SEQUENCE OF 1
TISSUE=Liver;
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                                                                                                     MEDLINE=20385067;
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Mammalia; Eutheria;
                                                                                                                              VARIANTS
                                                                                                                                                                                                                                     Houldsworth
                                                                                                                                                                                                                                                            MEDLINE=88124845; PubMed=2829183;
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                                                                                                                                                                                          dsworth J., Attardi G.;
distinct genes for ADP/ATP translocase
l in adult human liver.";
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                                                                                                                           PEO PRO-114 AND MET-289
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                                                                                                     PubMed=10926541;
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Primates;
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EXCHANGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nuclear genes for human mitochondrial
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, Suomalainen A.;
ocator 1 in mtDNA
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AND ATP
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                                                                                                                                                                                                               expressed
ACROSS THE
                                        maintenance.";
                                                                                 Zeviani
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Matches
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CONFLICT
SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00153; mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MITOCH_CARRI
PROSITE; PS00215; MITOCH_CARRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J02966; AAA61223.1; -.
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DISEASE: Defects in SLC25A4 are a cause of autosomal dominant progressive external ophthalmoplegia with various mitochondrial DNA deletions (PEO). Patients with PEO have mitochondrial myopathy, progressive external ophthalmoplegia, and other abnormalities associated with multiple different deletions of mitochondrial DNA.
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SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0006832; P:small molecule transport; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0006091; P:energy pathways; TAS.
GO:0000002; P:mitochondrial genome maintenance; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO:0005887; C:integral to plasma membrane; TAS GO:0005739; C:mitochondrion; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO:0015207; F:adenine transporter activity; TAS
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                                                                                                                                                      263;
              61
                                              51
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                                  I PKEQGVLS FWRGNLANVI RYF PTQALNFA FKDKYKQI FLGGVDKHTQFWRYFAGNLASG
              I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                             MGDHAWSFLKDFLAGGVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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                                                                                                                                                     Conservative
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Inner membrane; Repeat; Transmembrane; Transport;
ly; Disease mutation.
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149
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Pred. No. 2.1e-116;
9; Mismatches 16;
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Ffeiffer B.D.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Ffeiffer B.D.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Ffeiffer B.D.,
RA Barlew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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RA Dodson K.J., Bvangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
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RA Harris N.L., Harvey D., Helman T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Louvi A., Tsitilou s.v.,
"A cDNA clone encoding the ADP/ATP translocase
"A cDNA clone encoding the ADP/ATP translocase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
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Zhang Y.Q., Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hutter P., Karch F.; "Molecular analysis of a candidate gene for the reproductive isolation between subling species of Drosophila."; Experientia 50:749-762(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=7520869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roote J., Herrmann S., Ashburner the EMBL/GenBank/DDBJ databases.
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Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

Na Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Na Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

Na Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Na Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Na Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Na Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Na Nelson D.R., Nelson K.A., Nixon K., Scheeler F., Shen H.,

Na Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,

Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,

Narg Z.-v., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Walliams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Na Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,

"The genome sequence of Drosophila melanogaster.";

Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; $43651; AAB23114.1; -. EMBL; $71762; AAB31734.3; -. EMBL; $710618; CAA71628.1; -. EMBL; AX003484; AAP47957.1; -. EMBL; AX060978; AAL28526.1; -. EMBL; AX070894; AAL48516.1; -.
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STRAIN=Berkeley; TISSUE=Larva, Ovary, and Pupae;

MEDLINE=22426066; PubMed=12537569;

MEDLINE=22426066; PubMed=12537569;

Stapleton M., Carlson J.W., Brokstein P., Yu C., Char

George R.A., Guarin H., Kronmiller B., Pacleb J.M., I

Rubin G.M., Celniker S.E.;

"A Drosophila full-length cDNA resource.";

"A Drosophila full-length cDNA resource.";

Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
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GO; GC:0005743; C:mitochondrial inner membrane;
GO; GO:0006639; P:mitochondrial transport; IMP.
InterPro; IPR002067; Mit carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00153; mito_carr; 2.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3
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                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                               Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inner membrane (By similarity).
DOMAIN: Composed of three homologous domains.
SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Catalyzes the exchange of ADP and ATP a mitochondrial inner membrane.
SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pean Bioinformatics Institute. There are no rest
non-profit institutions as long as its content
and this statement is not removed. Usage by ar
regulires a license agreement (See http://www.isb-
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                                                             2 (POTENTIAL).
2 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
6 (POTENTIAL).
7 (IN REF. 1 AND 2).
7 (IN REF. 1).
8 (IN REF. 2).
9 (IN REF. 1).
1 -> P (IN REF. 2).
1 -> P (IN REF. 1).
1 -> P (IN REF. 1).
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                                                                                                                                                                                                                                                               Repeat; Transmembrane; Transport (POTENTIAL). (POTENTIAL). (POTENTIAL).
  D51F3E2A70BD59E8
                       S (IN REF. 1)
C (IN REF. 2)
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Liang Y.,
McPherson
  CRC64
                                                                                                                    AND 2).
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Lin X.,
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                                                                                                                        Pfam; PF00153; mito
PRINTS; PR00926; MIT
                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a content the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. The are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insc
Neoptera; Endopterygota; Diptera; Nematocera;
NCBI TaxID=7165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94348635; PubMed=8069414; Beard C.B., Crews-Oyen A.B., Kumar V.K.,
                                                                              PROSITE; PS002
Mitochondrion;
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InterPro; IPR001993; Mitoch_carrier.
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or send an email to license@isb-sib.ch).
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-!- SUBUNIT: Homodimer (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insect Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN:
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                                                                                                                                                                                                                        L11618; AAB04104.1;
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                                                    Inner membrane;
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                                                                                                  CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the mitochondrial carrier family.
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Pred. No. 7.5e-103;
Repeat; Transmembrane; (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL).
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EMBL; M76669; AAA33027.1; -.
PIR; A41677; A41677.
InterPro; IPR002067; Mit carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; Mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P31692;

101-JUL-1993 (Rel. 26, Created)

101-JUL-1993 (Rel. 26, Last sequence update)

15-JUL-1998 (Rel. 36, Last annotation update)

ADP,ATP carrier protein (ADP/ATP translocase)

translocator) (ANT).

Chlorella kessleri.
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TRANSMEM
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hilgarth C., Sauer N., Tanner W.,
"Glucose increases the expression of the
glyceraldehyde-1-phosphate dehydrogenase
J. Biol. Chem. 266:24044-24047(1991).
- FUNCTION: CATALYZES THE EXCHANGE OF A
MITOCHONDRIAL INNER MEMBRANE
- I. SUBUNIT: Homodimer (By similarity).
                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed: entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae;
Chlorellaceae; Chlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92084708; PubMed=1748677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3074;
                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                  inner membrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGGAAGATSLCFVYPLDFARTRLGADVGPGAGEREFNGLLDCLKKTVKSDGI IGLYRGFN
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TRANSMEM 45
TRANSMEM 108
TRANSMEM 151
TRANSMEM 209
TRANSMEM 248
TRANSMEM 304
SEQUENCE 339 3
                                                                                                                                                                                                                                                                                                                                                                                             ADT3 YEAST
P18238;
01-NOV-1990
                                                                                                                                                  Vissers S. Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                               YEAST
                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                    01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
ADP, ATP carrier protein 3 (ADP/ATP translocase translocator 3) (ANT 3)
AAC3 OR YBR085W OR YBR0753.
                                                               Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS
MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                         Andre B.,
                                                                                                                                                                                                                      MEDLINE=90324269; PubMed=2165073;
Kolarov J., Kolarova N., Nelson N.;
Kolarov J. translocator gene i
"A third ADD/ATP translocator gene i
J. Biol. Chem. 265:12711-12716(1990)
                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                            -!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Integral membrane
                                                                                                               STRAIN=S288c;
                                                                                                                           SEQUENCE OF 38-307 FROM N.A.
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
          DOMAIN: COMPOSED OF SIMILARITY: Belongs
                                    inner membrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IIIYRAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGSLLIVYPLDFARTRLAADVG-SGKSREFTGLVDCLSKVVKRGGPMALYQGFGVSVQG
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62 1 (POTENTIAL).
26 2 (POTENTIAL).
68 3 (POTENTIAL).
28 4 (POTENTIAL).
65 5 (POTENTIAL).
65 6 (POTENTIAL).
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            THREE HOMOLOGOUS DOMAINS. to the mitochondrial carrier
                                                                                                                                                                        Hein C., Jauniaux J.C., Urrestarazu
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5; Mismatches
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                                              Mitochondrial
             family
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SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -

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DT CHLRE STANDARD; FAL,

ID ADT_CHLRE STANDARD;

AC P27080;

AC P27080;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-CT-1994 (Rel. 30, Last annotation update)

DB ADP,ATP Carrier protein (ADP/ATP translocase) (A
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Best Local
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                                                                                 ABT. Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M34076; AAA97485.1; -.
EMBL; 235954; CAA85031.1; -.
PIR; A35582; A35582
SGD; S0000289; AAC3.
GG; GG:0005471; F.ATP/ADP antiporter activity; IMP.
GG; GG:0006854; P:ATP/ADP exchange; IMP.
InterPro; IPR002067; Mit carrier.
InterPro; IPR001993; Mitoch—carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institute. There are no restrictions modified and this statement is not removed. Usage by and for comentities requires a license agreement (See httn://www.y.and.for.com
       SEQUENCE FROM N.A.
STRAIN=FUD44-R2;
MEDLINE=93204887; PubMed=8455552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
TRANSMEM
                                                                  Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales.
Chlamydomonadaceae; Chlamydomonas.
                                                       NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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PRINTS; PR00926; MITOCHRER:
PROSITE; PS00215; MITOCH_CARR
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                                                                                                                                                                                                                                                                                            SVVGIVVYRGLYFGMFDSLKFLVLTGSLDGSFLAGFLLGWVVTTGASTCSYFLDTVRRRM
                                                                                                                                                                                                                                              MMTSGQA---VKYNGAIDCLKKIVASEGVGSLFKGCGANILRSVAGAGVISMYDQLQMIL
                                                                                                                                                                                                                                                                                                                   SVQGIIIYRAAYFGVYDTAKGM-LPDPKNTHIVVSWMIAQTVIAVAGVVSYPFDTVRRRM
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                                                                                                                                                                                                                                                                                                                                            AAGALSLLFVYSLDFARTRLAADAKSSKKGGARQFNGLTDVYKKTLKSDGIAGLYRGFMP
                                                                                                                                                                                                                                                                                                                                                                                           AKQEGLISFWRGNTANVIRYFPTQALNFAFKDKIKLMF--GFKKEEGYGKWFAGNLASGG
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53.7%;
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Pred. No. 4.5e
15; Mismatches
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RESULT 15
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ID ADT_S
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AC 01-NC
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Best Local
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Mitochondrion;
TRANSMEM 172
TRANSMEM 74
TRANSMEM 116
TRANSMEM 178
TRANSMEM 217
TRANSMEM 273
SEQUENCE 308
ADT_SCHPO STANDARD; PRT; 322 AA (209188; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) ADP_ATP carrier protein (ADP/ATP translocase translocator) (ANT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@jib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structure, evolution and expression of the mitochondrial ADP/ATP translocator gene from Chlamydomonas reinhardtii."; Mol. Gen. Genet. 237:134-144(1993).
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
-i- SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00153; mito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X65194; CAA46311.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAAGATSLCFVYPLDFARTRLAAD----VGKSGTEREFRGLGDCLVKITKSDGIRGLYQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIPKEQGVLSFWRGNLANVIRYPPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLAS 119
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                       (ADP/ATP translocase)
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Pred. No. 1.7e
55; Mismatches
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(POTENTIAL).
(POTENTIAL).
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1.7e-60;
81;
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                       (Adenine nucleotide
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RA Wood V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Comor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Comor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Holroyd S., Hormsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
James K., Jones M., Leather S., McLean J.,
RA James K., Jones M., Leather S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Griter K., O'Rell S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Bger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Geffeau A., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Daga R.R., Cruzado L., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RL Lock H., H., Combie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

"The graden C., Standard R., Standard C., Faller I., Neckons The Exchange OF ADP AND ATP ACROSS THE
C. -- FUNCTION EARLINES THE EXCHANGE OF ADP AND ATP ACROSS THE
                                                                                                                                 EMBL; Z49974; CAA90275.1; -.
EMBL; AL023634; CAA19176.1; -.
PIR; T40526; T40526.
GeneDB SPombe; SPBC530.10c; -.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; Mito_carr; 3.
PRINTS; PR00926; MITOCH_CARRIER; 2.
PROSITE; PS00215; MITOCH_CARRIER; 2.
    Mitochondrion; I
TRANSMEM 28
TRANSMEM 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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"Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).

Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 171:113-117(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inner membrane.
Inner membrane; Répeat; Transmembrane; Transport.
8 48 1 (POTENTIAL).
3 111 2 (POTENTIAL).
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241 263	182 203	124 143	8 6 4 4	7 26	Query Match Best Local & Matches 158	TRANSMEM TRANSMEM TRANSMEM TRANSMEM SEQUENCE
241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGWGGAFVLVLYDELK 295 : : : : :	182 OGIIIYRAAYEGVYDTAKG-MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPEDTVRRRMM	124 GATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV	64 EQGVLSFWRGNIANVIRYEPTQALNEAFKDKYKQIFLGGVDKHTQFWRYEAGNIASGGAA - - - - - -	7 SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPK 63 	Query Match 49.8%; Score 769; DB 1; Length 322; Best Local Similarity 53.6%; Pred. No. 3.3e-60; Matches 158; Conservative 50; Mismatches 75; Indels 12; Gaps	MEM 131 151 3 (POTENTIAL). MEM 197 217 4 (POTENTIAL). MEM 222 242 5 (POTENTIAL). MEM 289 309 6 (POTENTIAL). ENCE 322 AA; 35020 MW; 8AC3D16A40F41AFC CRC64;
	1 240	7 181 7 202	123	83	6,	

Search completed: December 18, Job time : 9.34267 secs 2003, 12:41:25

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0
seq length: 2000000000
A Geneseq 19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
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24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

98	4 N 0 L	321	Result
1391.5	1457.5 1442.5 1398.5	1553 1553 1553	Score
89.6	93.9 92.9 90.1	100.0 100.0 100.0	Query Match
298 298	298 298	297 297 297	Query Match Length DB
22	19 22 23	21 22 23	
AAU01199 AAU10379	AAW61169 ABU53219 AAO18516	AAY71031 AAU01198 AAU10378	ID
Human adenine nucl Human adenine nucl Human adenine nucl	Anti protein. Mus Human metabolism-a Human insulin rece	Human adenine nucl Human adenine nucl Human adenine nucl	Description

743	743	743	746	746	746	746	746	746	746	746	746	746	746	746	746	746	746	746.5	771	820	867.5	926.5	1101.5	1101.5	1147	1221.5	1241	1241	1268.5	•	•	•	•	1385.5	1385.5
47.8	47.8	47.8	48.0	48.0	œ	48.0	œ	48.0	ö	48.0	•	٠	٠	٠	٠	•	•	•	•	•	•	•	•	٠	•	•	٠	٠	81.7	٠	٠	•	89.2	89.2	89.2
381	363	346	1027	1009	992	381	381	381	381	363	363	363	363	346	346	346	346	379	301	298	222	228	315	315	307	263	299	299	429	325	323	298	298	298	298
21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	24	23	22	23	23	23	22	22	22	22	22	24	22	22	23	22	22	21
AAG17729	AAG17730	AAG17731	AAG38670	AAG38671	AAG38672	AAG38458	AAG37262	AAG37259	AAG36575	AAG38459	AAG37263	AAG37260	AAG36576	AAG38460	AAG37264	AAG37261	AAG36577	ABP81267	ABP73357	ABG18922	ABP74106	ABP43205	AAE21175	ABU53218	ABB58380	ABG27056	ABB67300	ABB66082	ABR41715	ABG15423	AAM41427	AAU10380	AAU01200	AAM39641	AAY71033
	Arabidopsis thalia		Arabidopsis thalia		Arabidopsis thalia					Arabidopsis thalia		Arabidopsis thalia	Ø	Arabidopsis thalia	00	Ø		Arabidopsis thalia		Novel human diagno	TRICH	Human ovarian anti	Human TRICH-19 pro	Human metabolism-a	Drosophila melanog	Novel human diagno	Drosophila melanog	Drosophila melanog		Novel human diagno	Human polypeptide	Human adenine nucl	Human adenine nucl	polypept	Human adenine nucl

ALIGNMENTS

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RESULT 1
AAY71031
ID AAY7
XX AAY7
AC AAY7
XX 29-A
XX Huma
XX H
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Human; adenine nucleotide translocator; ANTI; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; notropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; alzhelmer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome. dystonia;

Homo sapiens.

WO200026370-A2

11-MAY-2000

03-NOV-1999;

99WO-US25883.

03-NOV-1998; 08-SEP-1999; 98US-0185904. 99US-0393441.

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RESULT 2
AAUU118
IID AAUU
XX
AC AAUU
XX
DT 07-S
XX
DE Huma
XX
DR Huma
XX
MM Huma
XX
KW mitc
XW mitc
XW Alzh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           constructs. Any is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, disbetes, dystonia, cencephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
                                       Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin; mitochondrial permeability transition pore component; cell surviva
                                                                                               Human adenine nucleotide translocator-1 (ANT-1)
                                                                                                                                       07-SEP-2001
                                                                                                                                                                                                               AAU01198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease
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N-PSDB; AAD00519.
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                                                                                                                                                                                                                                                                                                                                                                                                                          QGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQ 240
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                                                                                                                                                                                                                 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                        QGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQ
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llarity 100.0%;
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Pred. No. 3.4e-173;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        produce adenine nucleotide translocator
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The present sequence represents human adenine nucleotide translocator-1 (C (ANT-1) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MFT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. ANT) fused to an energy transfer molecule (ETM) protein (c (e.g. ANT) fused to an alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MFT and/or cell survival. These agents are useful for the prevention or treatment of disease associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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N-PSDB; AAS05901.
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Velicelebi G,
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                                                                                                                                                                                                                                                                               GAAGATSLCFVYFLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
                                             SGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDBIKKYV
                                                                                                                                                 QGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQ 240
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SGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                         QGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQ
                                                                                                                                                                                                                         GAAGATSLCFVYPLDFARTRLAADV
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G, Davis R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders e.g. cancer, and deafness.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1553;
Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a recombinant expression construct (I) CC comprising a regulated promoter operably linked to a nuclect acid ce enoding an adenine nucleotide translocator (ANT) polypeptide. ANT cc enoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial CC matrix for ADP in the cytosol. (I) is useful for producing recombinant CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and CC culturing the host cell. (I) is also useful for targeting a polypeptide CC of interest to a mitochondrial membrane, where ANT polypeptide is CC expressed as a fusion protein with the polypeptide of interest. CC useful for identifying an agent that binds to an ANT polypeptide. ANT CC useful for identifying an agent that binds to an ANT polypeptide, CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating CC ANT from a biological sample, where the ANT ligand is covalently or non-cc covalently bound to a solid phase. Detectably labeled ANT ligand is also CC useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT1.
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Best Local S
Matches 297
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N-PSDB; AAS16688.
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                                121 GAAGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
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                                                                                                                                                                                                                                                                                MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                       .4e-173;
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MGDHAWSFLKDFLAGAVAAAVSKTAVAPISRVKLLLQVQHASKQISABKQYKGIIDCVVR

MGDQALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR

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                                                                 Query Match
                                                                                                                                                                                       The present sequence is the mouse Antl protein, the cDNA producing this polypeptide is cloned by screening a mouse heart cDNA library with the human Antl cDNA as a probe. The Antl cDNA sequence was determined by DNA raq dideoxy terminator cycle sequencing. The Antl protein is encoded by the Antl locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which can then be converted into ATP. An Antl homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Antl homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy, hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can be used to test possible therapeutic compounds which model increase/mediate ATP and ADP exchange across the mitochondrial membrane independent of ANT1.
                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mice lacking heart-muscle adenine nucleotide translocator protein useful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti; Adenine nucleotide translocator; cloning; screening; DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation; probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy; hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy; lactic acidosis; degenerative muscle disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 39-40; 61pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
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                           93.9%;
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Score 1457.5; DB 1
Pred. No. 5.4e-162;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                                            This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention.
                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example III; Page 850; 1095pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-327840/34.
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28-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene'therapy; vaccine; disease treatment; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human metabolism-associated DKFZphtes3_35n12 homologue #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-APR-2003
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                                             AWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKE
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   ALSPLKDPLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKE
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99US-0156503.
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                                                                                                                                                 92.98;
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                                                                                                                      Score 1442.5; DB
Pred. No. 3e-160;
0; Mismatches
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12-JAN-2001;
12-JAN-2001;
                                                                                                                                                                                                                                            12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
                                  Identifying an insulin receptor signaling modulator, useful as drug targets for treating diabetes or metabolic disorders, comprises contacting an assay system comprising insulin receptor signaling modifiers with a test agent -
                  Disclosure;
                                                                                                             Seidel-Dugan C,
                                                                                                                                                                                                        12-JAN-2001;
12-JAN-2001;
                                                                                                                                                                                                                          12-JAN-2001;
12-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human insulin receptor signaling modifier SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA018516;
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                                                                                                                                                                                                                                                                                                   12-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                           WO200255664-A2
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                        Human; insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                diabetes; metabolic syndrome; antidiabetic.
                                                                                            2002-599664/64.
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                                                                                                                               EXELIXIS
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                  Page 160-161; 232pp;
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2001US-261458P.
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                  English.
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The present invention relates to

a method

of identifying a candidate

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotetive; nootropic; antiParkinsonian; cytosteatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia, diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insulin receptor (INR) signaling modulating agent, involving contacting an assay system comprising an insulin receptor signaling modifier (ISM) polypeptide or nucleic acid with a test agent, and detecting a test agent-biased activity of the assay system. The method is useful for identifying candidate INR signaling modulating agents. ISM genes may be used as drug targets for treatment of disorders related to INR signaling such as diabetes or metabolic syndrome. ISM nucleic acids and polypeptides are useful for identifying and testing agents that modulate ISM function and for other applications related to the involvement of ISM in INR signaling, and for identifying subjects having a predisposition to such diseases associated with INR signaling. The present sequence is an ISM protein described in the exemplification of the invention.
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08-SEP-1999;
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Pred. No. 4.5e-155;
7; Mismatches 15;
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(MITO-) MITOKOR

Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin; mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

Human adenine nucleotide translocator-2 (ANT-2) protein.

07-SEP-2001

(first entry)

AAU01199

standard; Protein;

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AC AAUU
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DT 07-S
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DB Huma
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KW Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, mitochondrial diabetes, mitochondrial diseases, respectively, schizophrenia, mitochondrial diseases, respectively, respect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic against mitochondrial disease
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Ghosh SS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 AA;
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7; Mismatches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention on treatment of diseases associated with altered mitochondrial function or dysfunctional cells survival. These agents are useful for the prevention on dysfunctional cells associated with altered mitochondrial function or dysfunctional cells survival. These seemediates associated with altered mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents human adenine nucleotide translocator-2 (ANT-2) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 2; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule -
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Velicelebi G,
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241
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                                                                                                                                                                    121 GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
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                                                                                                                                                  GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                                                                                                IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                          MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                   OSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 296
                                                                                               VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTVRRRMM 239
                                                                                                                                                                                                                          I PKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKRTQFWRYFAGNLASG
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                                                                        VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPPDTVRRRMMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                     298
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3, Davis RE;
                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                                            Score 1391.5; DB 22;
Pred. No. 3e-154;
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RESULT 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cc conditions an adenine nuclectide translocator (ANT) polymeptide. ANT control of any synthesised in the mitochondrial control of ATP synthesised in the mitochondrial control of ATP synthesised in the mitochondrial control of any synthesised in the mitochondrial control of any synthesised in the mitochondrial control of any synthesised in the mitochondrial control of a synthesised as a fusion protein with the polymeptide is control of interest to a mitochondrial membrane, where ANT polypeptide is conserved as a fusion protein with the polypeptide of interest. CC expressed as a fusion protein with the polypeptide of interest. CC useful for identifying an agent that binds to an ANT polypeptide. ANT control is useful for determining the presence of an ANT polypeptide, control is useful for determining the presence of an ANT polypeptide. CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the presence of an ANT polypeptide. ANT control of the
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to nucleic acid encoding the polypeptide -
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Ghosh SS, Moos WH,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human adenine nucleotide translocator 2 (ANT2).
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                                                                                                                                                                                                                                                                                         1 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
                                                                                  GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMM
                                                  GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                                         IPKBQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                                                               I PKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                         MTDAALSFAXDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                           298 AA;
                                                                                                                                                                                                                                                                                                                                           Conservative
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Pei Y, Carroll AK;
                                                                                                                                                                                                                                                                                                                                              17,
                                                                                                                                                                                                                                                                                                                                           Score 1391.5; DB 23
Pred. No. 3e-154;
7; Mismatches 16;
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The patent discloses a method to produce adenine nucleotide translocator CC (ANT) proteins or ANT fusion proteins using recombinant expression CC constructs. ANT is a nuclear encoded protein and a major component of constructs and membrane. It mediates transport of adenosine CC di/tri-phosphates across the mitochondrial inner membrane and also serves CC as an important molecular component of the mitochondrial permeability CC transition pore, a modulator of apoptosis. ANT is used to identify agents CC or ligands that bind to, or interact with it. The ANT ligands are used to CC detect or isolate ANT in a biological sample, and therapeutically for CC regulating mitochondrial pore activity, for treating diseases associated CC with altered mitochondrial function, including Alzheimer's, Parkinson's CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic cepilepsy red ragged fibre syndrome. The present sequence is an calculation microtide transformation.
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                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-365619/31.
N-PSDB; AAD00521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anderson CM,
Ghosh SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-NOV-1998;
08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                          Claim 46; Page 173-174; 175pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY71033 standard; Protein; 298 AA
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                                      nucleotide translocator ANT3 from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davis
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99US-0393441.
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                                      human brain
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Sequence

Example 4;

SEQ ID NO 2786; 10078pp; English

such as central nervous Novel nucleic acids and WPI; 2001-442253/47. N-PSDB; AAI58797.

polypeptides, useful system injuries -

for

treating

disorders

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RESULT 11
AAM39641
ID AAM39642
AC AAM39
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Best Local Similarity
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25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0662191.

19-OCT-2000; 2000US-0693036.

29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                 Tang YT,
Wang J,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; chemokinetic; thrombolytic; drug screening; arthritis;
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                                                                                                                                                                                                 Liu C,
Wang Z,
Zhou P,
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Wehrman T,
Goodrich F
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Pred. No. 1.5e-153;
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Yang Y,
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                                                                                                                                                                                                                                                        Ren F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin; mitochondrial permeability transition pore component; cell surviva mitochondrial core component; mitochondrial related disorder; canc
                                                                                                                                                       03-NOV-1999;
                                                                                                                                                                                                                         03-NOV-2000; 2000WO-US30535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
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Note: The sequence data for this patent did not form part
                                                                             (MITO-) MITOKOR
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87.2%; Pred. No. 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ERM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as altahemer's disease, diabetes mellitus, Parkinson's disease. Huntinoton's disease, diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents human adenine nucleotide translocator-3 (ANT-3) protein. ANT proteins are mitochondrial permeability transition (MTD) pore components responsible mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deatness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Velicelebi G,
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241
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                                                                                                                                                          121
                                       240
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                                                                                                                                                                                                                                                                                                                                                 1 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                GAAGATSICFVYPIDFARTRIAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                           QSGRKGADIMYTGTVDCWRKIAKDEGAKAPFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                        VQGIIIYRAAYPGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM 239
                                                                                                                                                          GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                               IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
                                                                                                                                                                                                                                                                                                                       MTEQAISFAKDFLAGGIAAAISKTAVAPIBRVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                             VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                                                                                                                        I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig 2, 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      89.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RE;
                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1385.5;
Pred. No. 1.5e
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          .5e-153;
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                               298;
                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                               180
                                                                               240
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RESULT 13
AAU10380
ID AAU10
XX
AC AAU10
XX
AC AAU10
XX
TA + FE
XX
DT 14 - FE
XX
DE Human
XX
Human
XX
Human
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Human
XX
Human
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Human
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Human
XX
Human
                                                                                                                   AAU10380;
 Homo sapiens
                          mitochondrial
                                         Human;
                                                                Human adenine
                                                                                                                                             AAU10380 standard;
                                                                                           14-FEB-2002
                                        adenine nucleotide translocator;
                                                                                          (first entry
                            matrix
                                                                nucleotide translocator 3 (ANT3).
                                                                                                                                             Protein; 298
                          protein
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Murphy AN,

Clevenger W,

Wiley SE,

Andreyev AY,

Frigeri LG;

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RESULT 14
AAM41427
ID AAM41
XX
AC AAM41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant expression construct (I) C comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT C proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant CC MAT polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest.

CC Recombinant ANT polypeptide, or cells expressing the polypeptide. ANT cuseful for identifying an agent that binds to an ANT polypeptide. ANT cuseful for determining the presence of an ANT polypeptide. Preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating the presence of an antipolypeptide. ANT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
 AAM41427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide
                                  AAM41427 standard; Protein; 323 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 2; 147pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                              MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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                                                                                                                                                                                                                                                                                                                                                                                                         MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                             QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                                                                                                                                                                                              VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM 239
                                                                                                                                                                                                                                                                                                                                                        IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
                                                                                                                                                                                                                                                                 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                         QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                       I PKEQGVLSFWRGNLANVIRYPPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M, Davis
Moos WH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Pei Y, Carroll AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1385.5; DB 23; Length Pred. No. 1.5e-153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wiley SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for producing adenine nucleotide regulated promoter linked to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                               240
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Best Local (
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                       The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/hibhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang
Wang
Zhao
                                                                                                         Sequence
                                                                                                                                               C.N.S disorders.
Note: The sequence
                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotractic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                       Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-DEC-2000; 2000WO-US34263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia.
                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð, i
                                                    260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nootropic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                     2; SEQ ID NO 6358; 10078pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C,
Wang Z,
Zhou P,
                 MGDHAWSF1KDFLAGAVAAAVSKTAVAF1ERVK1LLQVQHASKQ1SAEKQYKG1IDCVVR
 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                           323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 2000US-0598042.
; 2000US-0620312.
; 2000US-0653450.
; 2000US-0662191.
; 2000US-0662191.
; 2000US-0693036.
; 2000US-0727344.
                                                    Conservative
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2000US-0552317.
                                                                                                           8
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Wehrman T, X
Goodrich R,
                                                                                                                                                  data
                                                                 89.2%;
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                                                                                                                                                for this patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen R,
                                                                  Score 1385.5; DB 2
Pred. No. 1.7e-153;
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                     English.
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Хие
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                                                                               DB 22;
                                                                                                                                                not form part
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Yang Y,
                                                     16;
                                                     Indels
                                                                               Length
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                                                                                323;
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                                                     Gaps
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RESULT 15
ABG15423
ID ABG15423
AC AC ABG15423
AC AC ABG15423
AC AC ABG15423
AC AC ABG15423
AC AC ABG15423
AC AC ABG15423
AC AC ABG15423
AC AC ABG15423
AC AC ABG15423
AC AC ABG15423
AC AC
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The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC quantitating expressed genes. (I) is useful in gene therapy techniques (CC for identifying expressed genes. (I) is useful in gene therapy techniques (CC for identifying expressed genes. (I) is useful in gene therapy techniques (CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical consisting of sites expressing (II). (I) and (II) are useful for treating (II) are useful fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 45782; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-639362/73
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23-AUG-2000; 2000US-0649167.
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Search completed: December 18, 2003, 12:40:46 Job time : 37.2542 secs

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

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US-09-1613-12
US-09-1613-565-2
US-08-518-8788-56
US-08-470-861A-51
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ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/434,354; CURRENT FILING DATE: 1999-11-03; NUMBER OF SEQ ID NOS: 54; SOPTWARE: FASTSEQ for Windows Version 3.0; SEQ ID NO 47; LENGTH: 297; TYPE; PRT; ORGANISM: Homo sapien
US-09-434-354-47
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Patent No. 6562563

GENERAL INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Miley, Sandra Eileen
APPLICANT: Miley, Sandra Eileen
APPLICANT: Frigeri, Luciano G.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AN
TITLE OF INVENTION: HORSELY AND METHODS FOR DETERMINING
THE REFERENCES: 660088.433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGDHAWSPLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQVKGIIDCVVR
                                   SGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                                                         QGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQ
                                                                                                                                                                                                                                                  GAAGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
                                                                                                                                                                                                                    GAAGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
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SGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                      QGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRWMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                            MGDHAWSFLKDFLAGAVAAAVSKTAVAFIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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Pred. No. 4.2e-172;
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US-08-961-871-10
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US-08-961-871-10
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                                                                                                                                                                                                                                                                                                                                                                                 Matches 279;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: MacGregor, Grant R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 60/030,017
FILING DATE: 01-NOV-1996
APPLICATION TOWNER: US 67/030,017
FILING DATE: 01-NOV-1996
APPLICATION TOWNER: US 60/030,017
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TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: lines
                                                                                                                                                                                                                                                                                                                                                                                                       Loca1
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OPERATING SYSTEM: PC-DOS/MS-DOS
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COUNTRY: US
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6013858
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                   QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                    VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM 239
                                                                                                                                                                                                                               I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDRHKQFWRYFAGNLASG
QSGRKGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 298
                                                                           VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMM
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                                                                                                                                                                                                                                                                                                                                                                             93.9%; Score 1457.5; DB 3;
93.6%; Pred. No. 5.4e-161;
93.6%; Orems B;
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US-09-434-354-48

RESULT 3

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APPLICANT: Murphy, Anne N.

APPLICANT: Millam
APPLICANT: Clevenger, William
APPLICANT: Alley, Sandra Elleen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Prigeri, Luciano G.
APPLICANT: Prigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
FILE REFERENCE: 660088.433
CURRENT APPLICATION NUMBER: US/9/434,354
CURRENT FILING DATE: 1999-11-03
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 49
LENGTH: 298
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APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
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; ORGANISM: Homo mapien
US-09-434-354-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 49, Application US/09434354
Patent No. 6562563
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LENGTH: 298
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS FILE REFERENCE: 660088.433 CURRENT FILLING DATE: 103/09/434,354 CURRENT FILLING DATE: 1099-11-03 NUMBER OF SEQ ID NOS: 54 NUMBER OF SEQ ID NOS: 54 SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Homo sapien
                                              ENGTH:
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; Pred. No. 2.5e-153;
17; Mismatches 16;
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US-09-996-243-289
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                                                        CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062186
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                         APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C13
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APPLICANT:
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OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/065311
OR FILING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/066770
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/075945
OR FILING DATE: 1998-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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5. 6478825
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Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGWGGAFVLVLYDEIKKYV
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Ferrara, Napoleone
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                                                                                                                                                                                                                                                                                                                                                                                           Napier, Mary A.
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art, Timothy A.
                                                                                                                                                                                                                                                                                                                                                             Nicholas F.
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Pred. No. 1.3e-152;
1; Mismatches 16;
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NUMBER: 60/
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PRIOR PRIOR

APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801

FILING DATE: 1998-06-18

APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089600

FILING DATE: 1998-06-17

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PRIOR

PILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952

LING DATE: 1998-06-19

APPLICATION NUMBER: 60/089948

APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089908 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18

FILING DATE: 1998-06-18

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APPLICANT: Strachan, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 1100.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 339
LENGTH: 469
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PRIOR FILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR APPLICATION NUMBER: 60/091978
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PRIOR APPLICATION NUMBER: 60/092182
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Patent No. 61505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GAAGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
62 PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDR-----HKQFWRYFAGN 116 : | : | : | : | : | ::
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                                                                                                                                               89;
                                                                                                    6 WSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVV----RI 61
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                                                                WRHL---VAGGGAGAVSRTCTAPLDRLKVLMQV-HASRSNNM----
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29.0%; Pred. No. 1.4e-26;
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090694
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695

APPLICATION NUMBER: 60/090678 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090690

FILING DATE: 1998-06-25

FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090676

FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542

APPLICATION NUMBER: 60/090540

FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090535
FILING DATE: 1998-06-24 PILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472

PILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 APPLICATION NUMBER: 60/090435 APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090429

1998-06-24

APPLICATION NUMBER: 60/090355 FILING DATE: 1998-06-23 FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23

FILING DATE: 1998-06-24

APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
FILING DATE: 1998-06-22

APPLICATION NUMBER: 60/090254

FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091544
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519

: 1998-07-01 NUMBER: 60/091519

FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091360

PILING DATE: 1998-0 APPLICATION NUMBER:

1998-06-26

60/090863

APPLICATION NUMBER: 60/090862

APPLICATION NUMBER:

60/090696

FILING DATE: 1998-06-25 FILING DATE: 1998-06-25

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RBSULT 7
US-09-312-283C-339
; Sequence 339, Application US/09312283C
; Patent No. 6573095
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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ORGANISM: Mouse
-09-312-283C-339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000 1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Watson, James D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                396
                                                                                                                                                                340
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454
                                                                                                                      228
                                                                                                                                                                                                                                                                                117 LASGGAAGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454
                                     287 LVLYDEIK 294
                                                                                                                                                                                                                                                                                                                            234 IREGGAKSLWRGNGINVLKIAPESAIKFMAYEQMKRLV--GSDQETLRIHER-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287 LVLYDBIK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 LVAGSLÁGÁTAQSSTYFMEVLKTRMÁL----RKTGQYSGMLDCARRÍLAKEGVAAFYKGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 IREGGAKSLWRGNGINVLKIAPESAIKFMAYEQMKRLV--GSDQETLRIHER-----
                                                                                                                                                                                                                                                                                                                                                                  62 PKBQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDR-----HKQFWRYFAGN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89;
                                                                                                                   YPFDTVRRRMMMQSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFV- 286
                                                                                                                                                            IPNMLGIIPYAGIDLAVYETLKNTWLQRYAVNSADP---GVFV-LLACGTISSTCGQLAS
                                                                                                                                                                                                  NVSVQGIIIYRAAYFGYYDTAKGM-----LPDPKNVHIFVSWMIAQSVTAVAG-LLS 227
                                                                                                                                                                                                                                                                                                                                                                                                          WRHL---VAGGGAGAVSRTCTAPLDRLKVLMQV-HASRSNNM-----CIVGGFTQM 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVV----RI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YPLALVRTRMQAQASIEGAPEVTMSSL--FKQILRTEGAFGLYRGLAPNFMKVIPAVSIS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I PNMLGI I PYAGI DLAVYETLKNTWLQRYAVNSADP---GVFV-LLACGTISSTCGQLAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LASGGAAGATSLCFVYPLDFARTRLAADVGRRAQRBFHGLGDCIIKIFKSDGLRGLYQGF 176
YVVYENLK 461
                                                                                                                                                                                                                                            LVAGSLAGAIAQSSIYPMEVLKTRMAL----RKTGQYSGMLDCARRILAKEGVAAFYKGY 339
                                                                              YPLALVRTRMQAQASIEGAPEVTMSSL--PKQILRTEGAPGLYRGLAPNFMKVIPAVSIS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YVVYENLK 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YPFDTVRRRMMQSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFV-
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Sleeman, Matthew
Onrust, Rene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.4%; Score 301; DB 4; Length 46
28.9%; Pred. No. 3e-26;
tive 64; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52;
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Sequence 4, Application US/09160119A
Patent NO. 6316219
GENERAL INFORMATION:
APPLICANT: KRIEF, STEPHANE
APPLICANT: BRIL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
CURRENT PILING DATE: 1998-09-24
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER PILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 4
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                                                                                                  TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-160-119-2
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                                                                                SOFTWARE:
SEQ ID NO 2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                 JENERAL INFORMATION:
APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHET, MICHEL
APPLICANT: BRIL, ANTOINE
                 LENGTH: 674
TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: HOMO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 NPLEIVKIRLQVAGEITTGPRVS------ALSVVRDLGFFGIYKGAKACFLRDIPFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 YPLDFARTRL--AADV--GRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 FLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISABKQYKGIIDCVVRIPKEQGFLSFW 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTTYSGVIDCFRKILREEGPKALWKGAGARVFRSSPQFGVTLLTYELLQRW 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAV-AGLLSYPFDTVRRRMMMQSGRKGA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGLLPQLLGVAPEKAIKLTVNDFVRDKFM-----HKDGSVPLAAEILAGGCAGGSQVIFT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSLCFV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIYFPCYAHVKASFANEDGQVSPGSLLLAGAIAGMPAASLVTPADVIKTR--LQVAARAG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGLGSVAGAVGATAVYFIDLVKTRMQNQRSTGSFVGELMYKNSFDCFKKVLRYEGFFGLY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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27.5%;
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Pred. No. 4.1e-25;
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RESULT

Best Local Similarity

27.5%;

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-501-558-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/501,558
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: No. 6403784el Human Uncoupling Proteins and TITLE OF INVENTION: Polynucleotides Encoding the Same FILE REFERENCE: LEX-0012-USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                            242 G-RKGADIMYTGTVDCWRKIAKDEGAKAPFKGAWSNVLR-GMGGAFVLVLYDEIKK 295
                                                                                        178 VELPVYDITKKHLILSGLMGDTVYTHFLSSF----TCGLAGALASNPVDVVRTRMMNQR
                                                                                                                                                                            122 TIANPTDVLKIRMQA----QSNTIQGGMIGNFMNIYQQEGTRGLWKGVSLTAQRAAIVVG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 AAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAV-AGLLSYPFDTVRRRMMQSGRKGA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            446 NPLEIVKIRLQVÄGEITTGPRVS------ALSVVRDLGFFGIYKGAKACFLRDIPFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 YPLDFARTRL--AADV--GRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 RGLLPQLLGVAPEKAIKLTVNDFVRDKFM-----HKDGSVPLAAEILAGGCAGGSQVIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331 FGLGSVAGAVGATAVYPIDLVKTRMQNQRSTGSFVGELMYKNSFDCFKKVLRYEGFFGLY 390
233 VLRDGRCSGYTGTLDCLLQTWKNEGFFALYKGFWPNWLRLGPWNIIFFVTYEQLKK 288
                                                                                                                                                                                                                        129 CFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYRA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
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                                                                                                                                                                                                                                                                       67 ALYSGIAPAMLRQASYGTIKIGTYQSLKRLF---IERPED--ETLPINVICGILSGVISS
                                                                                                                                                                                                                                                                                                                 69 SFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSL 128
                                                                                                                                                                                                                                                                                                                                                                                                    10 KDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQIS-ABKQYKGIIDCVVRIPKEQGFL 68
                                                                                                                                                                                                                                                                                                                                                               7
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                                                                                                                                  AYFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAG-LLSYPFDTVRRRWMMQS 241
                                                                                                                                                                                                                                                                                                                                                             KPFVYGGLASITAECGTFPIDLTKTRLOIQGQTNDAKFKEIRYRGMLHALVRIGREEGLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sands, Arthur T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Turner, C. Alexander Jr. Mathur, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zambrowicz, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.2%;
28.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 7.7e-25;
53; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 267; DB 4; Length 291; Pred. No. 1.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
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RESULT 11 US-09-482-273-118

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                                                                                                                                                                                                                                                                                                                            Sequence 12, Apparent No. 5932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Rosen et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 118, Application US/09482273 Patent No. 6534631
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NUMBER OF SEQ ID NOS: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US95/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: 71 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: PZ030P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1998-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE
LOCATION: (335)
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                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                               CORRESPONDENCE ADDRESS:
                                                                                                       APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                     APPLICANT:
STREET: 3174 POI
CITY: Palo Alto
                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 VGVELPVYDITKKHLILSGMMGDTILTH-----FVSSFTCGLÅGALASNPVDVVRTRMMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 ŚSTIANPTDVLKIRMQAQ-ĠSLFQGSMIG---SFIDIYQQEGTRGLWRGVVPTAQRAAIV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 VLALYSGIAPALLRQASYGTIKIGIYQSLKRLF---VERLED--ETLLINMICGVVSGVI 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 FLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGAT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            QRAIVGHVDLYKGTVDGILKMWKHEGFFALYKGFWPNWLRLGPWNIIFFITYEQLKR 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAAYFGYYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAG-LLSYPFDTVRRRMM 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIY 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GWGGAFVLVLYDEIKK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPFVYGGLASIVAEFGTFPVDLTKTRLQVQ--GQSIDARFKEIKYRGMFHALFRICKEEG 108
                                                                                                                                                                                                                                                                                                                                                  Application US/08933750C
                    B: Incyte Pharmaceuticals,
3174 Porter Drive
                                                                                                                                                                       Au-Young, Janice
Yue, Henry
                                                                                                                                                                                                                                        Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                    Shah, Purvi
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

Diskette

COUNTRY: USA

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                                                                                                                 Sequence 12, Application US/09234613 Patent No. 6132973
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                                                                                                                                                        -09-234-613-12
                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: SPLNN
CLONE: 207452
                                                             APPLICANT:
                                                                               APPLICANT:
                        APPLICANT:
                                            APPLICANT:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                                                                                                                                                                                                     303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 15.3%;
Similarity 23.5%;
                                                                                                                                                                                                                                     YE 304
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                                                                                                                                                                                                                                                                                                                   RLQVGGFEHARAAFGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFMFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VHPVDVLRTRFAA---QGEPKVYNTLRHAVGTMYRSEGPQVFYKGLAPTLIAIFPYAGLQ 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGHVPAQILSIGYGAVQFLSFEMLTELVHRGSVYDAREFSVHF----VCGGLAACMATLT 135
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                                                                                                                                                                                                                                                                                                                                                                                              FSCYSSLK-----
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                                    Lal, Preeti
Hillman, Jennifer
Bandman, Olga
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Shah, Purvi
Au-Young, Janice
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Pred. No. 3.6e-19;
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                                                             F
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RESULT 14 US-09-142-565-2

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; CLONE: 2
US-09-234-613-12
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SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,
FILING DATE: September 23, 19;
ATTORNEY JAGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 31. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: S
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APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: Sr. 207452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                     290
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 303
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                                                                                                                                                                                                                                                               131 VYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYRAAY 190
                                                                                                                                                                                                                                                                                                      80
                                                                                                                                                                                                                                                                                                                                      72 RGNLANVIRYFPTQALNF-AFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSLCF 130
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                                                                                                                                                                                                                                                                                                                                                                                                                   13 LAGAVAAAVSKTAVAPIERVKLLLQVQHAS-KQISAEKQYKGIIDCVVRIPKEQGFLSFW 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                             VAGSVSGLVTRALISPFDVIKIRFQLQHERLSRSDPSAKYHGILQASRQILQEEGPTAFW
                                     YD 291
                                                                          RLQVGGFEHARAAFGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFMFFS 302
                                                                                                            RMMM---QSGRK--GADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GMGGAFVLVL 289
                                                                                                                                                                                                                            VHPVDVLRTRFAA---QGEPKVYNTLRHAVGTMYRSEGPQVFYKGLAPTLIAIFFYAGLQ 192
                                                                                                                                                                                                                                                                                                    KGHVPAQILSIGYGAVQFLSFEMLTELVHRGSVYDAREFSVHF----VCGGLAACMATLT 135
YE 304
                                                                                                                                               FSCYSSLK-----HLY-KWAIPAEGKKNENLQNLLCGSGAGVISKTLTYPLDLFKK
                                                                                                                                                                                      FGVYDTAKGMLPDPKNVHIFVSWMI -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 238; DB 3; 1; pred. No. 3.6e-19; 67; Mismatches 124;
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RESULT 15
US-08-518-878B-56
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 56, Application US/08518878B Patent No. 5702902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.0%; Score 233.5; DB 3; Best Local Similarity 24.7%; Pred. No. 1.2e-18; Matches 73; Conservative 53; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: HOMO SAPIEN
-09-142-565-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 9705614.7
EARLIER FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: 97305305.1
EARLIER FILING DATE: 1997-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL COMPOUNDS
                      SOPTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/518,878B
                                                                                  ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                           NUMBER OF SEQUENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Pennie & Edmonds
Pennie & Edmonds
Pennie of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 312
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tartagli
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                        STATE: New York COUNTRY: U.S.A.
  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ĕ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 ---NSPPGQYFSPLDCMIKMVAQEGPTAFYKGFTPSFLRLGSWNVVMFVTYEQLKR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GMGGAFVLVLYDEIKK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 YRAAYFGVYDTAKGMLEDPKNVHIFVSWMIAQSVTA----VAGLLSYPFDTVRRRMMMQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 TCAQPTDVVKVRFQASIHLGPSRSDRKYSGTMDAYRTIARBEGVRGLWKGTLPNIMRNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 CFVYPLDFARTRLAADV---GRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIII 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/142,565A
FILING DATE: 1999-06-30
APPLICATION NUMBER: 9704551.2
FILING DATE: 1997-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2, Application US/09142565A
5. 6187560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEK--QYKGIIDCVVRIPKEQGFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYNGLVAGLOROMSFASIRIGLYDSVKOVYTPKGADNSSLTTRILA-----GCTTGAMAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLGAGTAACFADLVTFFLDTAKVRLQIQGENQAVQTARLVQYRGVLGTILTMVRTEGFCS
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                                                                                                                                                                                                                                                                                                                                                                                      Tartaglia,
23-AUG-1995
                                                                                                                                                                                                                                                                                                                                            COMPOSITIONS AND METHODS FOR THE TREATMENT OF BODY WEIGHT DISORDERS,
                   US/08/518,878E
                                                                                                                                                                                                                                                                                                                                                                                      Louis A.
                                                                #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 14.6%; Score 227; DB 1; Length 299
Best Local Similarity 23.8%; Pred. No. 6.2e-18;
Matches 70; Conservative 52; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
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                                                                                       182 AELVTYDLIKDALLKANLMTDDLPCH-FTSAFGAGFCTTV---IASPVDVVKTRYM----
                                                                                                                                   189
                                                                                                                                                                            122 AVAQPTDVVKVRFQAQARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVNC 181
234 -NSALGOYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKR
                                                                                                                                                                                                                        129 CFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGIIIYRA 188
                                                                                                                                                                                                                                                                    67
                                                                                                                                                                                                                                                                                                           69 SFWRGNLANVIRYFFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATSL 128
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                                                                                                                                                                                                                                                                                                                                                         7
                                       RKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLR-GMGGAFVLVLYDEIKK
                                                                                                                                                                                                                                                                                                                                                       FLGAGTAACIADLITFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMGTILTMVRTEGPR 66
                                                                                                                              AYFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQSG 242
                                                                                                                                                                                                                                                                 SLYNGLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHAS----IGSRLLAGSTTGALAV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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Search completed: December 18, 2003, 12:44:54
Job time: 13.3057 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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1553
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                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA:*

1: /cgn2 6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2-6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2-6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
/ Cgm2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                       -6/ptodata/2/pubpaa/PCTUS PUBCOMB.pep:*
-6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
-6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
-6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Match Length DB		ID	Description
–	1553	100.0	297	9	US-09-811-094-31	Sequence 31, Appl
2	1553	100.0	297	9	US-09-810-644-31	Sequence 31, Appl
w	1553	100.0	297	10	US-09-185-904A-31	Sequence 31, Appl
4.	1391.5	89.6	298	9	US-09-811-094-32	Sequence 32, Appl
ۍ.	1391.5	89.6	298	9	US-09-810-644-32	Sequence 32, Appl
ტ	1391.5	89.6	298	10	US-09-185-904A-32	Sequence 32, Appl
7	1385.5	89.2	298	9	US-09-811-094-33	Sequence 33, Appl
80	1385.5	89.2	298	ø	US-09-810-644-33	Sequence 33, Appl
9	1385.5	89.2	298	10	US-09-185-904A-33	Sequence 33, Appl
10	773.5	49.8	179	12	US-10-029-386-32501	Sequence 32501, A
11	771	49.6	301	12	US-10-032-585-7194	Sequence 7194, Ap
12	740	47.6	381	12	US-10-141-478A-2	Sequence 2, Appli
13	734	47.3	318	10	US-09-801-368-252	Sequence 252, App
14	734	47.3	386	ø	US-09-734-569-170	Sequence 170, App
15	703.5	45.3	308	15	US-10-128-714-3338	Sequence 3338, Ap

45	44	4	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	
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US-09-989-734-289	US-09-993-687-289	US-09-990-436-289	US-09-989-730-289	US-09-991-181-289	US-09-990-444-289	US-09-989-735-289	US-09-989-293A-289	US-09-992-598-289	US-09-989-721-289	US-09-990-456-289	US-09-993-604-289	US-09-991-163-289	US-09-990-442-289	US-09-991-073-289	US-09-989-732-289	US-09-989-731-289	US-09-989-727-289	US-09-989-279-289	US-09-989-723-289	US-09-989-722-289	US-10-291-172-339	US-09-777-921A-5	US-10-094-749-1789	US-09-777-921A-2	US-09-777-921A-4	US-09-864-761-36440	US-09-925-301-1459	US-10-259-165-192	
289,	289,	Sequence 289, App	289,	289,	e 289,	289,	289,	Sequence 289, App	289,	289,	289,	289,	289,		e 289,	e 289,	289,	289,		Sequence 289, App	Sequence 339, App	Sequence 5, Appli			Sequence 4, Appli	Sequence 36440, A		Sequence 192, App	

ALIGNMENTS

120 120	Qy 61 IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG	
60	Cy I MSDHAWSELKDELAGAVAAAVSKTAVAFIEKVKLLLQVQHASKQISAEKQYKGIIDCVVK	
	Query Match 100.0%; Score 1553; DB 9; Length 297; Best Local Similarity 100.0%; Pred. No. 2.3e-160; Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps	
	; ORGANISM: Homo sapien US-09-811-094-31	
	LENGTH: 297	
	; SOTTWARE: FastSEQ for Windows Version 3.0	
	NUMBER OF SEQ ID NOS: 37	
	; CURRENT APPLICATION NUMBER: US/09/811,094	
	; TITLE OF INVENTION: NOVEL ANT LIGANUS AND SCREENING ASSAUS THEREFOR ; FILE REFERENCE: 660088.420D4	
	OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE	
	; APPLICANI: MOOB, Walter H. ; APPLICANI: Pei, Yazhong	
	: Ghosh,	
	: Willer, Scott	
	; APPLICANT: Clevenger, William ; APPLICANT: Wiley, Sandra Bileen	
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	; GENERAL INFORMATION:	
	; Patent No. US20010044144A1	
	; Sequence 31, Application US/09811094	
	US-09-811-094-31	
	RESULT 1	

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US-09-185-904A-31; Sequence 31, Application US/09185904A; Patent No. US20020177185A1
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US-09-810-644-31
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APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Moos, Walter H.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
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Best Local S
Matches 297
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CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PRT
ORGANIEN: Homo sapien
S-09-810-644-31
                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31, Application US/09810644 Patent No. US20020012992A1
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Clevenger, William
Wiley, Sandra Eileen
Willer, Scott W.
Szabo, Tomas R.
Szabo, Tomas R.
Ghosh, Soundter H.
Pell, Yazhong
Pell, Yazhong
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                                                                                                                                                                Anderson, Christen M.
Davis, Robert E.
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100.0%; Pred. No. 2.3e-160;
tive 0; Mismatches 0;
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Davis, Robert E.

APPLICANT: Clevenger, William
APPLICANT: Willey, Sandra Eileen
APPLICANT: Willey, Sandra Eileen
APPLICANT: Szabo, Tomas R.
APPLICANT: Szabo, Tomas R.
APPLICANT: Hosh, Sounitra S.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D4
CURRENT APPLICANTON NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D4
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastsEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
GRANISM: Homo sapien
US-09-811-094-32
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APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
ITILE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND TITLE OF INVENTION: THEREFOR PILE REFREENCE; 660088.420
CURRENT FAPLICATION NUMBER: US/09/185,904A
CURRENT FALING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien
US-09-185-904A-31
100.0%; Score 1553; DB 10; Length: Companism of the compa
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APPLICANT: Davis, Robert B.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Elleen
APPLICANT: Wiler, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
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US-09-810-644-32
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CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
                                                                                                                                                                                                                                                                                                                                                                              Query Match 89.6%; Score 1391.5; DB 9; Best Local Similarity 88.6%; Pred. No. 8.3e-143; Matches 263; Conservative 17; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapien
3-09-810-644-32
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Patent No. US20020012992A1
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                                                                                                         VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM 239
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CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
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                                                                                                                                                                                                                                                                                                                                    Sequence 33, Application US/09811094 Patent No. US20010044144A1
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Best Local Similarity 88.6%;
Matches 263; Conservative 1
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APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiler, Scott W.
APPLICANT: Wiler, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFY
FILE REFERENCE: 660088.42004
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
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APPLICANT:
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TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: THEREFOR
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: Willer, Scott W.
: Szabo, Tomas R.
: Ghosh, Soumitra S.
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Pred. No. 8.3e-143;
Pred. Nismatches 16; II
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; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-33
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US-09-810-644-33
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APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Bileen
APPLICANT: Wiler, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 66008 420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
                                                                                                                                                                                                   Query Match 89.2%; Score 1385.5; DB 9
Best Local Similarity 87.2%; Pred. No. 3.7e-142;
Matches 260; Conservative 21; Mismatches 16;
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Best Local Similarity 87.2%; Pred. No. 3.7e-142;
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ORGANISM: Homo sapien
-09-810-644-33
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                                                                                                                                                                                                                                           DB 9;
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US-10-029-386-32501

US-10-029-386-32501; Sequence 32501, Application US/10029386; Publication No. US20030194704A1; GENERAL INFORMATION:
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; ORGANISM: Homo sapien
US-09-185-904A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-185-904A-33
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SEQ ID NO 33
LENGTH: 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity Matches 260; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LITTLE OF INVENTION: THEREFOR
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                                                                                                                                                                                                                                                                  QSGRKGADIMYTGTVDCWRKIAKDBGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                                                                                                                                                                                                                                                                                                      GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  İPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Davis, Robert
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87.2%;
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Pred. No. 3.7e-142;
11; Mismatches 16; I
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FILE REFERENCE: AEOMICA-X-2

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TYPE: PRT
CORGANISM: Candida albicans
US-10-032-585-7194
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US-10-032-585-7194
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CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 7194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7194, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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LENGTH: 179
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APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Boone
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
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NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers.
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96
OTHER INFORMATION: SWISSPROT HIT: P05141, EVALUE 2.00e-83
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Local Similarity 88.3%; Pred. No. 6.7e-76;
es 144; Conservative 12; Mismatches 6
                                                                                    126
    183
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                                                                                 TSLCFVYPLDFARTRLAADVGRR----AQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQG 182
                                                                                                                                                 GFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                                           NFFVDFMMGGVSÅÅVSKTAAAPIERVKLLIQNQDEMIKQGRLEKRYTGIVDCFKRTAADE
                                                                                                                                                                                                                                   SFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQ-HASKQISAEKQVKGIIDCVVRIPKEQ 65
IIIYRAAYFGVYDTAKG-MLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMQS 241
                                                                                                                           GVVSFWRGNTANVIRYFPTQALNFAFKDKFKAMF--GFKKDENYWKWFAGNLASGGLAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IFLGGVDKRTQFWLYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGL
                                       TSLAFVYSLDYARTRLANDAKSSKGDGKREFNGLVDVYKKTLASDGIAGLYRGFGPSVIG 182
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                                                                                                                                                                                                                                                                                             49.6%; Score 771; DB 12;
53.9%; Pred. No. 2.5e-75;
tive 43; Mismatches 82
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RESULT 13 US-09-801-368-252

GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Cali, Brian

Robert

APPLICANT:

Hecht, Peter Holtzman, Dou

Sequence 252, Application US/09801368 Patent No. US20020128250A1
GENERAL INFORMATION:

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; ORGANISM: Arabidopsis thaliana
US-10-141-478A-2
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US-10-141-478A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10141478A Publication No. US20030148300A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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APPLICANT: Savage, Thomas
APPLICANT: Voelker, Toni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/289,519
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/289,527
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: TO Be Assigned,
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Voelker, Toni
APPLICANT: Zang, Wei
TITLE OF INVENTION: Metabolite Transporters
FILE REFERENCE: 16515.146
CURRENT APPLICATION NUMBER: US/10/141,478A
CURRENT FILING DATE: 2002-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
369
                                  294
                                                                                                                                                                                                                               196
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                                                                                                                                                                                       180 VQGIIIYRAAYFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVR 234
                                                                                                                                                                                                                                                                                                           137 DEGFGSLWRGNTANVIRYFFTQALNFAFKDYFKRLFNFKKDR-DGYWKWFAGNLASGGAA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165;
                                                                                                                                                                                                                                                                                                                                      64 EQGFLSFWRGNLANVIRYFFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAA 123
                                                                                                                                                                                                                                                                                                                                                                                    79 NFALDFIMGGVSAAVSKTAAAPIERVKLLIQNQ--DEMIKAGRLSEPYKGIGDCFGRTIK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381
                                                                                                                                                                                                                                                                                                                                                                                                                7 SFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISA---EKQYKGIIDCVVRIPK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn version 3.0
                                                                                                                                                                                                                                                     GATSLCFVYPLDFARTRLAADVGRRAQ----REFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQA---VKYDGALDCFRKVVAAEGVGSLFKGCGANILRGVAGAGVISLYDQLQ 292
LIVEGKKY 376
                                                                                                            RRMMMQSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEI- 293
                                                                                                                                                  CVGIIVYRGLYFGLYDSVKPVLLTGDLQD----SFFASFALGWVITNGAGLASYPIDTVR
                                                                                                                                                                                                                               GASSLLFVYSLDYARTRLANDAKAAKKGGGGRQFDGLVDVYRKTLKTDGIAGLYRGFNIS 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGWGGAFVLVLYDBIK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----KKY 296
                                                                        RRMMMTSNEA---VKYKSSLDAFKQILKNEGAKSLFKGAGANILRAVAGAGVLSGYDKLT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
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Pred. No. 8.1e-72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 381;
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LENGTH: 318
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                Sequence 170, Application US/09734569
Patent No. US20020064816A1
                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                    APPLICANT: Lerchl, Jens
APPLICANT: Renz, Andreas
APPLICANT: Ehrhardt, Thomas
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APPLICANT: Silva, Jeff
APPLICANT: Silva, Jeff
APPLICANT: Summers, Bric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
TITLE OF INVENTION: Moss genes from Physcomitrella patens TITLE OF INVENTION: in the synthesis of carbohydrates FILE REFERENCE: BASF-NAS-1332-99-US CURRENT APPLICATION NUMBER: US/09/734,569 CURRENT FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 60/171,101 PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GOA---VKYDGAFDCLRKIVAAEGVGSLFKGCGANILRGVAGAGVISMYDQLQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVVYRGLYFGMYDSLKPLLLTGSLEGSFLASFLLGWVVTTGASTCSYPLDTVRRRMMTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIIYRAAYFGVYDTAKGMLPDPKNVHIFV-SWMIAQSVTAVAGLLSYPFDTVRRRWMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSLLFVYSLDYARTRLAADSKSSKKGGARQFNGLIDVYKKTLKSDGVAGLYRGFLPSVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVISFWRGNTANVIRYFPTQALNFAFKDKIKAMF--GFKKEEGYAKWFAGNLASGGAAGA
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                                                                                                                            Duwenig, Elke
Schmidt, Ralf-Michael
Reski, Ralf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Milne,
                                                                                                                                                                Freund, Annette
Duwenig, Elke
                                                                                                                                                                                                      Frank, Markus
                                                                                                                                                                                                                     Bischoff, Friedrich
                                                                                                                                                                                                                                                         Reindl, Andreas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Madden,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Royer, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No. US20020128250Alman,
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Pred. No. 2.8e-71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82;
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                                                                                                         encoding proteins involved
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7 SFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISA---EKQYKGIIDCVVRIPK 63

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US-10-128-714-3338
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US-10-128-714-3338
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                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR PILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR PPLICATION NUMBER: US 60/295,890
PRIOR PILING DATE: 2001-06-05
PRIOR PPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 170
LENGTH: 386
                                                                                                                                                    SOPTWARE: PatentIn version 3.1
SEQ ID NO 3338
LENGTH: 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3338, Application US/10128714 Publication No. US20030119013A1
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Best Local Similarity 52.9%;
Matches 156; Conservative 43
  Matches 150;
                      Best Local Similarity
                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jiang, APPLICANT: Hu, W
                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/316,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 10182-018-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                   LENGTH: 308
TYPE: PRT
ORGANISM: Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 GMMSLWRGNTANVIRYFPTQALNFAFKDYFKSLF--GYKKDKDGYWKWFAGNLASGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 GELSFWRGNLANVIRYPPTQALNFAFKDKYKQLFLGGVDRHKQ-FWRYFAGNLASGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 SFWTDFLMGGVSAAVSKTAAAPIERVKLLIQNQDEMLKSGRLSHPYKGIGECFSRTVKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 SFLKOFLAGAVAAAVSKTAVAPIERVKLLLQVQ-HASKQISAEKQYKGIIDCVVRIPKEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hu Wengi
Tishkoff, Daniel
Zamudio, Carlos
Eroshkin, Alexey M
Lemieux, Sebastien M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATSLCFVYPLDFARTRLAADVGRR----AQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGIIVYRGLYFGIYDSLKPVVLVGNLEGNFLASFLLGWGITIGAGLASYPIDTVRRRMM
45.3%; Score 703.5; DB 15, 50.8%; Pred. No. 5.7e-68; ive 45; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1/WordPerfect 6.1
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                                              DB 15;
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        Indels
                                              Length
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        13;
        Gaps
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8	64 EQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAA 123
Вb	65 AEGVMSLWRGNTANVIRYFPTQALNFAFRDTYKSMFAYKKDR-DGYAKWMMGNLASGGAA 123
9	124 GATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
Db 1	124 GATSLLEVYSLDYARTRLANDAKSAKGGGERQENGLIDVYRKTLASDGIAGLYRGEGESV 183
φ. 1	181 QGIIIYRAAYEGVYDTAKG-MLEDDKNVHIEVSWMIAQSVTAVAGLLSYPEDTVRRRMM 239
Db 1	184 LGIVVYRGLYFGMYDSIKÞVVLVGSLEGSFLASFLLGWTVTTGAGIASYPLDTIRRRMM 243
Qy 2	240 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGWGGAFVLVLYDEIK 294
Db 2	244 TSGEAVKYKSSLDAARQIIAKEGVKSLFKGAGANILRGVAGAGVLSIYDQVQ 295
Search comp Job time :	Search completed: December 18, 2003, 12:55:43 Job time : 25.2788 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prir and is derived by analysis of the total score distribution.
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21.1	21.5	22.2	22.5	22.6	23.4	23.7	23.7	32.7	43.5	46.3	46.9	46.9	47.2	47.3	47.4
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ALIGNMENTS

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F:5-99/Domain: ADF,ANF CARRIER PROCEST REPEAT NOMOLOGY CACELS	D ATT CATTIET OF
F;2-298/Product: ADP,ATP carrier protein #status predicted <mat></mat>	P, ATP carrier pr
C; Keywords: duplication; homodimer; mitochondrion; transmembrane protein	P,ATP carrier pr
C,Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology	P,ATP carrier pr
A)CLOBETECRETICES: GUD:LIYGOV) CMIM:LU3ZZV	notherical prote
A-dene: GDB:ANT1; T1	P,ATP carrier pr
C;Genetics:	P,ATP carrier pr
A; Experimental source: liver	P, ATP carrier pr
A;Cross-references: GB:J03593; NID:g339724; PIDN:AAA36751.1; PID:g339725	p/atp translocas
A;Residues: 1-37 <hou></hou>	P,ATP carrier pr
A; Molecule type: mRNA	P, ATP carrier pr
Alphanetion Alalia Astroj murocatatotoj marocatato	pothetical prote
A; Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a	P,ATP carrier pr
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988	pothetical prote
R;Houldsworth, J.; Attardi, G.	pothetical prote
A; Experimental source: clone pHMANT	pothetical prote
A;Cross-references: GB:J02966; NID:g339919; PIDN:AAA61223.1; PID:g339920	pothetical prote
A:Residues: 1-15.'A'.17-146.'RR'.149.151-226.'L'.228-298 <nec></nec>	P,ATP carrier pr
A. Wolecule type: mRNA A. MOLECULE type: mRNA	P.ATP carrier pr
A. Crafting area in in a service and the control of	D ATD Carrier pr
A:Accession: A39891	P.ATP carrier pr
A) ILLE: CUMM BEQUEICE OI MUITO BOALLAGI MUBGIE ADF/AIF CIGHBLOCACOI: IACK OI & IEAGEI A.Deference number: A19801 MUITO-80A11140: DMTD-292786	P.ATP Carrier or
PTOC. Nati. Acad. Sci. U.S.A. 84, 7580-7584, 1987. N. ATTI G. LEDNA securings of a human civiletal muscle and/or translocator. lack of a leader	r, Air carrier pr
K;NeCKeLmann, N.; L1, K.; Wade, K.F.; Snuster, K.; Wallace, U.C.	enine nucleotide
	WALE CARRIER PR
A; Molecule type: DNA	
A;Status: not compared with conceptual translation	scription
A; Accession: S03893	
A, Reference number: \$03893; MUID:89236396; PMID:2544251	
A: Title In. DNA seminance of two control of the seminance of the seminance of the transfer of the seminance of two controls and the seminance of two controls of the seminance of two controls of the seminance of two controls of the seminance of two controls of the seminance of two controls of the seminance of two controls of the seminance of two controls of the seminance of two controls of the seminance of two controls of the seminance of two controls of the seminance of two controls of the seminance of two controls of t	
T MOI BIOL 2016 261-280 1080	IOII.
A;Cross-references: GB:J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659	being printed,
A;Residues: 1-298 <lia></lia>	to have a
A; Molecule type: DNA	
A;Status: preliminary	
A,Accession: A44778	
A; it-re: A numen muscle agenthe nucleoride translocator gene has rour exons, is located. A:Reference number: A44778; MUID:R9340499; PMID:S2447778	
J. B101. Chem. 264, 13998-14004, 1989	
R;Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.	
C; Accession: A44778; S03893; A39891; A28116	
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000	
C; Species: Homo sapiens (man)	
N; Alternate names: mitochondrial ADP, ATP translocase 1	
ADP ATP carrier protein T1 - human	
A44778	

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C;Accession: I60173
R;Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
R;Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
Biochim. Biophys. Acta 1152, 192-196, 1993
A;Title: Isolation and characterization of cDNA clones a
A;Reference number: I60173; MUID:94002161; PMID:8399300
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein
C;Keywords: duplication; transmembrane protein
C;Keywords: ADP,ATP carrier protein repeat homology <ACP1>
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QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGWGGAFVLVLYDEIKKYV
                                                                                                  VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM 239
                                                                                                                                                                                 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
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ADP, ATP carrier protein repeat homology <ACP3>
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Pred. No. 4.1e-125;
9; Mismatches 7;
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Pred. No. 1.5e-130;
2; Mismatches 2;
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S37210
ADP,ATP carrier protein T1 - mouse
ADP,ATP carrier protein T1 - mouse
N,Alternate names: adenine nucleotide carrier
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-195 #sequence_revision 06-Jan-19
C;Accession: S37210
R;Laplace, C.; Costet, P.
submitted to the EMBL Data Library, September 19
A;Reference number: S37210
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-298 <LAP>
A;Residues: 1-298 <LAP>
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A;Renetics:
A;Genetics:
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C;Genetics:
C;Genetics: ANC1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homo C;Superfamily: ADP,ATP carrier protein
C;Superfamily: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-203/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                             A;Molecule type: mRNA
A;Residues: 1-298 <POW>
A;Residues: 1-298 <POW>
A;Residues: 1-298 <POW>
A;Cross-references: GB:M24102; NID:g529414; PIDN:AAA30768.1
A;Cross-references: CB:M24102; NID:g529414; PIDN:AAA30768.1
B;Cosserver (Commun. 138, 850-857, 1986
B;Cochem. Biophys. Res. Commun. 138, 850-857, 1986
A;Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two
A;Reference number: A24822; MUID:86295775; PMID:3017341
                                                                                                                                                                                                                   C;Species: Bos primigenius taurus (cattle)
(;Date: 14-Nov-1983 #sequence revision 22-Jul-1994 #text_change
C;Accession: A43646; A24822; A03181; A61343; S69369
R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Blochemistry 28, 866-873, 198
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase
A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Accession: A43646
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                                             A;Accession: A24822
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    ;Molecule type: mRNA
;Residues: 208-298 <RAS:
                                                                                                                                                                                                                                                                                                                                                                                                   DP,ATP carrier protein T1 - bovine
;Alternate names: ADP/ATP translocase
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                                                                                                                                                        NID:g529414; PIDN:AAA30768.1;
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Pred. No. 7.6e
10; Mismatches
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A;Accession: Aballa
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 205-298 <BAB>
R;Oettmeier, W; Masson, K.; Kalinna, S.
R;Oettmeier, Wasson, K.; Kalinna, S.
Bur. J. Biochem. 227, 730-733, 1995
Bur. J. Biochem. 227, 730-733, 1995
A:Title: [(3)H]7-azido-4-isopropylacridone labels Cys159
A:Title: [(3)H]7-azido-4-isopropylacridone labels Cys159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Comment: This protein is synthesized in the cytosol and transported into the mic;Complex: homodimer
C;Complex: homodimer
C;Complex: homodimer
C;Complex: homodimer
C;Function:
A;Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATF
A;Note: located in the inner mitochondrial membrane
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homodimer; methylated amino acid;
F;Seywords: acetylated amino end; duplication; homodimer; methylated amino acid;
F;59/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;10-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;207-Modified site: acetylated amino end (Ser) (in mature form) #status experiment
F;52/Modified site: N6-methyllysine (Lys) #status predicted
ADP,ATP carrier protein T2 - human
NJP,ATP carrier which is growth-regulat
NJP,ATITLE: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulat
NJP,ATP carrier protein T2 - human
NJP,ATP carrier which is growth-regulat
NJP,ATP carrier which is growth-regulat
NJP,ATP carrier which is growth-regulat
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NJP,ATP carrier which is growth-regulat
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R;Babel, W.; Wachter, E.; Aquila, H.; Klingenberg, M.
Biochim. Biophys. Acta 670, 176-180, 1981
A;Title: Amino acid sequence determination of the ADP,ATP
A;Reference number: A61343; MUID:82046808; PMID:6271240
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A; Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298
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;Residues: 49-63;154-168 <OET>
;Comment: This protein is syntl
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Pred. No. 2.2e-124;
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ADP,ATP carrier protein T3 - human
N,Alternate names: ADP,ATP carrier protein T2
C,Species: Homo sapiens (man)
C,Date: 17-Mar-2000 "-
A; Molecule type: mRNA
A; Residues: 36-104,'R',106,'A',109-298 <HOU>
A; Cross-references: GB: J03592; NID: 9339722; 1
A; Experimental source: liver
                                                                                                   R;Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase are
A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: B28116
                                                                                                                                                                                                                                                                                         A;Reference number: S03893; MUID:89236396; PMID:2541251 A;Accession: S03894
                                                                                                                                                                                                                                                                                                                                                   R;Cozens, A.L.; Runswick, M.J.; Walker, J. Mol. Biol. 206, 261-280, 1989
A;Title: DNA sequences of two expressed
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A; Molecule type: mRNA
A; Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
A; Cross-references: GB.J03591; NID:g339720; PIDN:AAA36749.1;
A; Cross-references: Glone pHAT3
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Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase are
A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: C28116
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A; Residues: 1-298
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A;Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
                                                                                                                                                                                                                                                                            A;Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                              ;Species: Homo sapiens (man)
;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change
;Accession: S03894; B28116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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                                                                                                                                                                                                                             1-298 <COZ>
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Pred. No. 2.5e-118;
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                          PIDN: AAA36750.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (misidentification); mitochondrial
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C;Species: BOS primited C;Date: 03-Mar-1993 #Sequence_revision: C;Date: 03-Mar-1993 #Sequence_revision: C;Accession: B43646
R;Powell, S.U.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A;Pitle: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in A;Pitle: Two bovine genes for mitochondrial primited Pitle: Two bovine genes differently in A;Reference protein; ADP,ATP carrier protein repeat homology carrier protein primitochondrial; transmembrane protein primitochondrial; transmembrane protein primitochondrial; ADP,ATP carrier protein repeat homology carrier protein protein repeat homology carrier protein protein repeat homology carrier protein protein repeat homology carrier protein protein repeat homology carrier protein protein repeat homology carrier protein protein repeat homology carrier protein protein repeat homology carrier protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein pr
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A;Cross-references: GDB:125184; OMIN:300151; OMIM:403000
A;Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A;Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;2-298/Product: ADP,ATP carrier protein repeat homology AACP1>
F;10-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;110-203/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
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87.2%; Pred. No. 8.8e-118;
87.2%; Mismatches 16;
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A;Accession: S31935
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <BEA>
A;Crose-references: EMBL:Z21814; EMBL:Z21815
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier C;Keywords: duplication; transmembrane protein
C;Keywords: duplication; protein repeat homology
                                                                                                                                                                          ADP, ATP carrier protein - African malaria mosquito (;Species: Anopheles gambiae (African malaria mosquito) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text (;Accession: $31935; $31936 R;Beard, C.B., Crews-Oyen, A.E.; Collins, F.H. submitted to the EMBL Data Library February 1993 A,Description: A cDNA encoding an ADP/ATP carrier from 1,Reference number: $31935
                                                                                                                                                                                                                                                                                                                                                                RESULT
S31935
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein;
C;Superfamily: ADP,ATP carrier protein
C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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C;Date: 06-Jan-1995 #sequence_revision
C;Accession: S31814
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGWGGAFVLVLYDEIKKY 296
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87.2%;
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C;Species: Caenornawuru.
C;Date: 15-Oct-1999 #sequence_revision 15-Ucu-1999
C;Accession: T25850
R;Gelsel, C: Stellyes, L.
submitted to the EMBL Data Library, December 1996
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A; Introns: 4/1; 191/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U80931; PIDN:AAB38001.1; GSPDB:GN00022; CESP:T01B11.4
A;Experimental source: strain Bristol N2; clone T01B11
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A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: Z20099
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene: CESP:T01B11.4
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Best Local Similarity
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263
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                         DIMYTGTVDCWRKIAKDEGAKAPFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                             AAYEGMEDTAKOVVETADGKKLNEEAAWALAQVVTVGSGILSYEWDTVRRRMMMQSGRK--
                                                                                                                                                                                                              LSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                             FLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKEQGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKEQ
DVLYKNTLDCAVKIIKNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKFI
                                                                                             AAYFGVYDTAKGML-PDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRKGA
                                                                                                                            LCFVYPLDFARTRLAADVGKANEREFKGLADCLVKIAKSDGPIGLYRGFFVSVQGIIIYR
                                                                                                                                                                                            AALWRGNLANVIRYFPTQALNFAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                                                                          FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASLTIAADKRYKGIVDVLVRVPKEQGY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIK 294
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                                                                                                                                                                                                                                                                                                                       67.3%; Score 1045.5; DB 2; 69.8%; Pred. No. 5.6e-87; Live 36; Mismatches 49;
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                                                                          A; Map position: 3
A; Introns: 20/1; 41/3;
C; Superfamily: ADP, ATP
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T23207
                                                                                                                                                                                                       A;Status: preliminary; translated A;Molecule type: DNA
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                                                                                                                          A; Gene: CESP: T27E9.1
                                                                                                                                                                                           A; Residues: 1-300 <WIL>
                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                          R;Lloyd, C.
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hypothetical protein T2789.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T25371
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A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat
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                                                                                                                                                                                                 A;Cross-references: EMBL:Z82059; PIDN:CAB04874.1; A;Experimental source: clone T27E9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDE
A;Molecule type: DNA
A;Residues: 1-313 <WIL>
A;Cross-references: EMBL:Z68218; PIDN:CAA92472.1;
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                                                                                      115/2 carrier protein;
                     66.8%; Score 1037.5; DB 2; 69.1%; Pred. No. 2.8e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.2%; Score 1043.5; DB 2; 69.4%; Pred. No. 8.5e-87;
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                                                                                        ADP, ATP
                                                                                        carrier protein
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ADP,ATP carrier protein - Chlorella kessleri
C;Species: Chlorella kessleri
C;Date: 30-Jun-1992 #sequence_revision 30-Ju
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C; Superfamily: I
F; 9-103/Domain:
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A;Residues: 1-300 <LET>
A;Cross-references: EMB
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A; Accession: T15206
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C;Accession: T15206
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C;Species: Caenorhabditis elegans
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#sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
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ce: strain Bristol N2; clone W02D3
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-301 <HAT>
A;Cross-references: EMBL:X83551; NID:g623334; PIDN:CAA58541.1; PID:g623335
A;Cross-references: EMBL:X83551; NID:g622334; PIDN:CAA58541.1; PID:g623335
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein
C;Keywords: duplication; transmembrane protein
F;6-102/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;112-203/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;209-301/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: ADP/ATP transporter C;Species: Plasmodium falciparum C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-J. C;Accession: S68993; SS1132 R;Hatin, I.; Jaureguiberry, G. Bur. J. Biochem. 228, 86-91, 1995 Bur. J. Biochem. 228, 86-91, 1995 A;Title: Molecular characterisation of the ADP/ATP-transporter cDNA A;Reference number: S68993; MUID:95188918; PMID:7883016 A;Accession: S68993
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S51132
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R;Hilgarth, C.; Sauer, N.; Tanner, W.
B;Hilgarth, C.; Sauer, N.; Tanner, W.
J. Biol. Chem. 266, 24044-24047, 1991
A;Title: Glucose increases the expression of the ATP/ADP translocator and A;Reference number: A41677; MUID:92084708; PMID:1748677
A;Accession: A41677
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP, ATP carrier protein - malaria parasite
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QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG 124
                                                                             SFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISA--EKQYKGIIDCVVRIPKE
                                                   KGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDBIKKYV
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                                                                                                                                                      Score 904.5; DB 2;
Pred. No. 3.1e-74;
18; Mismatches 70;
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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.W., Green	n A., Young A.C., She	Hale S., Ga Sodergren	cKernan K.	., Toshiyu	Bonaldo M.	oore T., Ma	Buetow K.	E.A., Grous	2477932;		.A. 04: /00	and coevolution with mitochondrial DNA gr	gence from	R.P., Shue	PubMed=2823266:	4004 (1989)	, and is d:	himizu Y.,	J.A., Minos		1887)		Runswick M.J., Walker J.E.; es of two expressed nuclear	PubMed=2541251;			ta; Craniata; V		cleotide t	heart/skeletal muscle	sequence 1	ted)	PRT;		ALIGNMENTS	CMC1_DRO	UCP5 MOUSE	CMC2_MOU	CMC2 HUMAN MFT HUMAN	GDC RAT	CMC2_CAEEL	
E.D., Dickson M.C	VA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	<pre>arcia A.M., Gay L.o B.J., Lu X., Gibb</pre>	J., Malek J.A., Gu	ci S., Carninci P.	.F., Casavant T.L.	ax S.I., Wang J.,	i., Schaefer C.F.,	se L.H., Derge J.G)-/304(130/).	enes.";	broblast	R., Wall		•	ifferentially expressed	Pukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace	shima S., Kudoh J.				genes	l		nominicae;	ertebrata;		۳	isof	update)		298 AA.		MENTS			-		•	•	
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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MIM; 103220; --
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GO; GO:0005887;
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GO; GO:0000001;
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EMBL; J04982; AAA51736.1; -.
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PIR; A44778; A44778.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 289:782-785(2000).
-i- FUNCTION: CATALYZES THE EXCHANGE OF MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                            Pfam; PF00153; mito carr; 3. PRINTS; PR00926; MITOCARRIER. PRINTS; PR00784; MTUNCOUPLING
                                                                                                                                                                                                     InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
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Kaukonen J., Juselius J.K., Tiranti V., Kyttala A.,
Comi G.P., Keranen J., Peltonen L., Suomalainen A.;
"Role of adenine nucleotide translocator 1 in mtDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad.
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                                                                                                    TRANSMEN
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                                                                                                                                                                                                                                               GO:0005887; C:integral to plasma membrane; TAS. GO:0005739; C:intechondrion; TAS. GO:0005739; C:intechondrion; TAS. GO:0015207; F:adenine transporter activity; TAS. GO:0006091; F:energy pathways; TAS. GO:000002; P:mitochondrial genome maintenance; TAS. GO:0006832; P:mmall molecule transport; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
DISBASE: Defects in SLC25A4 are a cause of autsochal dominant progressive external ophthalmoplegia with various mitochondrial DNA deletions (PEO). Patients with PEO have mitochondrial myopathy, progressive external ophthalmoplegia, and other abnormalities associated with multiple different deletions of mitochondrial DNA.

SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Integral membrane
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. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
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                                                                                                                                                                                                                                                                                                                                                                      HGNC:10990; SLC25A4.
                                                                                                                                              PS00215; MITOCH_CARRIER;
                                                                                                                  family;
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176
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                        This SWISS-PROT entry is copyright. It is processed to the Elbetween the Swiss Institute of Bioinformatics and the Elbetween the Swiss Institute. There are no rest to the same of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the con
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                                                                                                                                                                                                                                                                                                                         Shinohara Y., Kamida M., Yamazaki N., Terada H.;
"Isolation and characterization of cDNA clones and a genomi encoding rat mitochondrial adenine nucleotide translocator. Biochim. Biophys. Acta 1152:192-196 (1993).

-I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
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                    modified and
                                                                                                                                                                       STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, MEDLINE=94002161; PubMed=8399300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLC25A4 OR ANT1.
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                                                                                                                                                   DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                    SUBUNIT: Homodimer
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G -> A (IN REF. 3).

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requires a license agreement (See http://www.isb-sib.ch/announce.

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Matches
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homologs.";
Mamm. Genom
[2]
                                                                                                                                    ADTI_MOUSE STANDARD; PRT; 298 AA. P48962; Q62164; O1-FEB-1996 (Rel. 33, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) ADP_ATP carrier protein, heart/skeletal muscle translocase 1) (Ademine nucleotide translocator SIC25A4 OR ANTI OR ANCI.
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                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=97059403; PubMed=8903
                                                                                                                                                                                                                               MOUSE
                                                                                                          Bukaryota; Metazoa;
Mammalia; Eutheria;
                                            Ellison J.W.,
                                                                                             NCBI_TaxID=10090;
                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X61667; CAA43842.1;
EMBL; D12770; BAA02237.1;
PIR; I60173; I60173.
                               Ellison J.W., Li X., France "Rapid evolution of human
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PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
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            Genome
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                                          PubMed=8903724;
K., Francke U.,
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Rodentia;
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                               pseudoautosomal genes
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Pred. No. 4.7e-124;
9; Mismatches 7;
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Sciurognathi; Muridae;
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                                          Shapiro L.J.;
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Murinae; Mus
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 EMBL; U27315; AAC52837.1; -.
EMBL; X74510; CAA52616.1; -.
EMBL; AP240002; AAF64470.1; -.
EMBL; BC003791; AAH03791.1; -.
EMBL; BC003791; AAH03791.1; -.
EMBL; BC026925; AAH26925.1; -.
PIR; S37210; S37210.
MCD; MGI:1353495; S102584.
InterPro; IPR002007; Mtt_carrier.
InterPro; IPR002030; Mtt_uncoupling.
InterPro; IPR001993; Mitoch carrier.
                                                               Mitochondrion;
Multigene famil
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PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                              Pfam; PF00153; mito
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Repeat; ω

Transmembrane;

Transport;

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RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Rabin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carrinat P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton R., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M.,
RODRIGUEZ A.C., Grimwood J., Schmutz J.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M.,
Rodriguez A.C., Grimwood J., Schmutz J.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M.,
RA Rodriguez A.C
                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C., "Expression and sequence analysis of the mouse ad translocase 1 and 2 genes.", "Language" (Cantant/Inna, dat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laplace C., Costet P.;
Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases
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STRAIN=BALB/c; TISSUE=Muscle;
Laplace C., Costet P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane
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an email to license@isb-sib.ch).
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RESULT 4
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ADT1 B
ADT1 B
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01-JUL-1993 (Rel. 26,
16-OCT-2001 (Rel. 40,
                                                                                                                                            an unusually short 3'-noncoding sequence."
Biochem. Biophys. Res. Commun. 138:850-857
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADI
                                                                                                                                                                                                              MEDLINE=86295775; PubMed=3017341;
Rasmussen U.B., Wohlrab H.;
"Bovine cardiac mitochondrial ADP/ATP-carrier: two
                                                                                                                                                                                                                                                                                                                                                      "Complete amino mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=82188267; PubMed=7076130;
Aquila H., Misra D., Eulitz M., Klingenberg M.;
"Complete amino acid sequence of the ADP/ATP carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry 28:866-873 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89229093; PubMed=2540808; Powell S.J., Medd S.M., Runswick M.J., "Two bovine genes for mitochondrial AD differences in various tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLC25A4 OR ANT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-UUI-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart isoform T1 (ADP/ATP translocase (Adenine nucleotide translocator 1) (ANT 1).
                                                                                                                                                                                                                                                                                   SEQUENCE OF
                                                                                                                                                                                                                                                                                                                              Hoppe-Seyler's Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
inner membrane.

DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

SIMILARITY: Belongs to the mitochondrial carrier family
                                                                            SUBCELLULAR LOCATION:
                                                                                                   SUBUNIT: Homodimer
                                                                                                                      MITOCHONDRIAL INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOVIN
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Pred. No. 8.7
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Best Local
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Multigene famil;
INIT MET 1
MOD RES 1
MOD RES 51
TRANSMEM 11
TRANSMEM 116
TRANSMEM 116
TRANSMEM 175
TRANSMEM 175
TRANSMEM 175
TRANSMEM 213
TRANSMEM 272
                                                           DDT2 MOUSE STANDARD; PRT; 298 AA. P5188]; Q61311; Q613
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M13783; AAA30363.1; -.
EMBL; M24102; AAA30768.1; -.
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PR00784; MITOCH CARRIER; 3.
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Pred. No. 6.8e-123;
Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                                                                                            (ADP/ATP
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Query Match
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                                                                                                                        TRANSMEM
TRANSMEM
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EMBL; U10404; AAA19009.1; -.
EMBL; X70847; CAA50196.1; -.
EMBL; AF240003; AAF64471.1; -.
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Submitted
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                                                                    REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                 InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PP00153; mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
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                                                   SEQUENCE
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                                                                                                                                                                                                                                                   Mitochondrion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20432087; PubMed=10974536; Levy S.E., Chen Y.-S., Graham B.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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TISSUE=Skeletal muscle;
Sheldon J.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97059403; PubMed=8903724;
Ellison J.W., Li X., Francke U., Shapiro L.J.;
"Rapid evolution of human pseudoautosomal genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buropean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: CATALYZES THE EXCHANGE MITOCHONDRIAL INNER MEMBRANE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the ER European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                  PR00784; MTUNCOUPLING.
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Score 1408.5; DB 1;
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MBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                "Isolation and characterization of cDNA clones and a genomic encoding rat mitochondrial adenine nucleotide translocator."; Biochim Biophys. Acta 1152:192-196(193).
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS TH MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADT2 RAT
Q09073;
                                                                                  InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                 EMBL; D12771; BAA02238.1; InterPro; IPR002067; Mit_
                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Sprague-Dawley; TISSUE-Liver; MEDLINE-94002161; PubMed-8399300; Shinohara Y., Kamida M., Yamazaki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, fibroblast isoform (
(Adenine nucleotide translocator 2) (ANT 2).
               PROSITE; PS00215; MITOCH CARRIER; 3
Mitochondrion; Inner membrane; Repea
                                          PRINTS; PR00926; MITOCARRIER. PRINTS; PR00784; MTUNCOUPLING
                                                                                                                                                                                       use by non-profit institutions as long as modified and this statement is not removed. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                      between
                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY:
SKELETAL MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                 DOMAIN:
                                                                                                                                                                                                                                                                                                                                          inner membrane.
                                                                         PF00153; mito
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                                                                                                                                                                                                                                                                                               THREE HOMOLOGOUS DOMAINS
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                                                                                                                                                                                                                yright. It is produced through a collaboration of Bioinformatics and the EMBL outstation of Biotitute. There are no restrictions on its
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Sciurognathi; Muridae; Murinae; Rattus.
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               Repeat;
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               Transmembrane;
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13-AUG-1987 (Rel. 05, O
01-OCT-1994 (Rel. 30, I
28-FEB-2003 (Rel. 41, I
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MEDLINE-90375457; PubMed=2168878;
MEDLINE-90375457; PubMed=2168878;
MEDLINE-90375457; PubMed=2168878;
MEDLINE-POSTATE

KERNEY

The human fibroblast adenine nucleotide cloning and sequence.";
Cloning and sequence.";
Cloning and sequence.";
J. Biol. Chem. 265:16060-16063(1990).
                                     SEQUENCE FROM N.A.
Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraja R.,
Mazzarella R.A., Schlessinger D., Chen E.Y.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                        growth-regulated
J. Biol. Chem 2
                                                                                                                                                                 "Molecular cloning
                                                                                                                                                                                                                         Battini
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Mammalia; Eutheria;
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Pred. No. 9e-
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9e-119;
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Best Local Sim
Matches 264;
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                                                                                                                                                                                                                                                                                                           PRINTS; PRO0926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
PROCEITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. Then use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See For send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc.
                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005887; C:integral to plasma membrane; TAS. GO; GO:0015207; F:ademine transporter activity; TAS. GO; GO:0006832; P:small molecule transport; TAS. InterPro; IPR002067; Mit_carrier. InterPro; IPR002030; Mit_uncoupling. InterPro; IPR001993; Mitoch_carrier.
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EMBL; J02683; AAA35579.1; -.
EMBL; L78810; AAB39266.1; -.
EMBL; AC004000; AAB96347.1; -.
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PUNCTION: CATALYZES THE EXCHANGE OF ADP ANI
MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: Homodimer.
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             IPKEQGFLSFWRGNLANVIRYFFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
                                           MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
  I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKRTQFWRYFAGNLASG
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to the EMBL/GenBank/DDBJ databases
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Pred. No. 5.8e-118;
7; Mismatches 15;
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                                                                                                                               V -> L (IN REF. 2).
G -> E (IN REF. 2).
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V -> G (IN REF. 5).
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RA Altacher R.D., Collins P.S., Wagner L., Schamen C.M., Schuler G.D.,
RA Altacher R.D., Collins P.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altacher R.D., Collins P.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altacher R.D., Collins P.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Rillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Muzny G., Shevchenko Y., Bouffard G.G.,
RA Makesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M.,
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01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADP,ATP carrier protein, liver isoform T2 (ADP/ATP translocase (Adenine nucleotide translocator 3) (ANT 3).
SLC25A6 OR ANT3.
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ADT3_I
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Margolin J.F.;
Submitted (JUL-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=89236396; PubMed=2541251;
Cozens A.L., Runswick M.J., Walker J.E.;
"DNA sequences of two expressed nuclear genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa;
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01-OCT-1989 (Re
Houldsworth J., Attardi G.;
"Two distinct genes for ADP/ATP translocase ar
level in adult human liver.";
Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988)
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AN
MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                         MEDLINE=88124845;
                                                                                                                                            SEQUENCE OF 3
TISSUE=Liver;
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n J.F.;
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                                                                                                                       PubMed=2829183;
                                                                                                                                                             FROM N.A
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EMBL; BC008935;
EMBL; BC014775;
PIR; S03894; S03
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CONFLICT
SEQUENCE
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InterPro; IPR0101993; Mitoch carrier.
Pfam; PF00153; mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00926; MITOCARRIER.
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InterPro; IPR002030; Mit_uncoupling.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (Supersend an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00215; MITOCH CARRIER;
Mitochondrion; Inner membrane; Rep
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DOMAIN: COMPOSED OF
SIMILARITY: Belongs
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L; AY007135; AAG01998.1; -.
L; BC007295; AAH07295.1; -.
L; BC007850; AAH07850.1; -.
L; BC008737; AAH08737.1; -.
L; BC008935; AAH08935.1; -.
L; BC014775; AAH14775.1; -.
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Pred. No. 8.4e-117;
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S -> F (IN REF. 3; AAH14775)
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Best Local Similarity
Matches 259; Conser
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01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation T2 (ADP/ATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89229093; PubMed=2540808; Powell S.J., Medd S.M., Runswick M.J., "Two bovine genes for mitochondrial AD! differences in various tissues."; Biochemistry 28:866-873(1989).
                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupil
InterPro; IPR001993; Mitoch_carri
InterPro; IPR001993; Mitoch_carri
Pfam; PF00153; Mito_carr; 3.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP, ATP carrier protein, isoform T2 nucleotide translocator 3) (ANT 3). SLC25A6 OR ANT3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the mitochondrial carrier family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane
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                                                 MTEQAISFAKDPLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                              MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
I PKEQGVLS FWRGNLANVIRY F PTQALNFAFKDKYKQI FLGGVDKRTQFWRY FAGNLASG
                       I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
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Pred. No. 2.4
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P/ATP translocase expressed
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Addams M.D., Celliker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celliker S.B., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.B., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Baxter B.G., Helt G., Wilson C.R., Miklos G.L.G.,
RA Bartl J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu B., Center A., Chandra I.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Posler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADT_DROME STANDARD; PRT; 299 AA. Q26365; P91614; Q26354; Q95S30; Q9VZ70; Q26365; P91614; Q26354; Q95S30; Q9VZ70; Q26365; P21614; Q26354; Q95S30; Q9VZ70; Q26365; P21614; Last sequence update) 15-SEP-2003 (Rel. 42, Last sequence update) ADP,ATP carrier protein (ADP/ATP translocase) (Advision (ADP/ATP translocator) (ANT) (Stress sensitive B protein). SESB OR A/A-T OR CG15944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular analysis of a candidate gene for the reproductive isolation between sibling species of Drosophila."; Experientia 50:749-762(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Louvi A., Tsitilou S.G.,
"A cDNA clone encoding the ADP/ATP translocase
"A cDNA clone encoding the ADP/ATP translocase
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MEDLINE=92389367; PubMed=1387687;
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databases.
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ARA Lasko P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshersi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittuan G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RI Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                   EMBL; $43651; AAB23114.1; -.

EMBL; $71762; AAB31734.3; -.

EMBL; $710618; CAA71628.1; -.

EMBL; AB003484; AAF47957.1; -.

EMBL; AV070894; AAL28526.1; -.

EMBL; AV070894; Cimitochondrial inner membrane; IE; GO; GO:0006734; Cimitochondrial transport; IMP. InterPro; IPR0012067; Mit carrier.

InterPro; IPR001993; Mitoch carrier.

Pfam; PF00153; mito_carr; 2.

PRINTS; PR00153; mito_carr; 3.

PROSITE; PR00215; MITOCH_CARRIER; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Berkeley; TISSUE=Larva, Ovary, and PuMEDLINE=22426066; PubMed=12537569; Stapleton M., Carlson J.W., Brokstein P., Yu George R.A., Guarin H., Krommiller B., Pacle Rubin G.M., Celniker S.E.; "A Drosophila full-length cDNA resource."; Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.6.1- PUNCTION: Catalyzes the exchange of ADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Catalyzes the exchange of ADP mitochondrial inner membrane. SUBUNIT: Homodimer (By similarity). SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: Composed of three homologous domains. SIMILARITY: Belongs to the mitochondrial carrier family.
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MISSING (IN REF. 1)
G -> A (IN REF. 2)
TG -> P (IN REF. 1)
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2 (POTENTIAL).
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                      S (IN REF. 1).
C (IN REF. 2).
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P (IN REF. 1 AND
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Anopheles gambiae (African malaria mosquito).
Authropoda, Hexapoda; Insecta,
Eukaryota, Metazoa, Arthropoda, Nematocera, Culic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed.
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Beard C.B., Crews-Oyen A.E., Kumar V.K.,
"A CDNA encoding an ADP/ATP carrier from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthi
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-I- SUBBUNIT: HOmodimer (by similarity).
-I- SUBCELLULAR LOCATION: Integral membrane
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                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed; entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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-i- FUNCTION: CATALYZES THE EXCHANGE OF A MITOCHNUBRIAL INNER MEMBRANE.
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10-JUL-1993 (Rel. 26, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation up
15-JUL-1998 (Rel. 37, Last annotation up
15-JUL-1998 (Rel. 37, Last annotation up
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                           Pfam; PF00153; mito_carr; PRINTS; PR00926; MITOCARRI
                                                                                                                    EMBL; M76669; AAA330:
PIR; A41677; A41677.
                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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Chlorellaceae; Chlorella.
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Chlorella kessleri.
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                                                                     InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
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TRANSMEM 304
SEQUENCE 339;
                     This SWISS-PROT entry is copyright. It is produced through a complete the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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01-AUG-1992 (Rel. 23, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation updat
ADP,ATP carrier protein (ADP/ATP translocas
translocator) (ANT).
                                                                                                                                                                                                  Sharpe J.A., Day A.;
"Structure, evolution and expression translocator gene from Chlamydomonas Mol. Gen. Genet. 237:134-144(1993).
-I- FUNCTION: CATALYZES THE EXCHANGE
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                                                                                                                                                                                                                                                                                                                                Chlamydomonadaceae;
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Bukaryota; Viridiplantae; Chlorophyta;
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EMBL; X65194; CAA46311.1;
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                                                                                                                                                               MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Integral membrane
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                                                                                                                                                    membrane
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Pred. No. 7.6e-80;
0; Mismatches 65
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STRAIN=CV. B3/N;
MEDLINE=B9338399; PubMed=2547608;
Leaver C.J., Bathgate B., Baker A.;
Leaver C.J., aroode the adenine nucleotide translocator
                                                                               SEQUENCE C
                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-MUTIND-FR7205034;
MEDLINE-91322533; PubMed=1863785;
Winning B.M., Day C.D., Sarah C.J.
"Nucleotide sequence of two cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1987 (Rel. 05, Created)
01-AUG-1992 (Rel. 23, Last sequence
16-OCT-2001 (Rel. 40, Last annotati
ADP,ATP carrier protein 1, mitcohon
translocase 1) (Adenine nucleotide
ANT1 OR ANT-G1.
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InterPro; IPR001993; Mitoch_carrier.
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S; PR00926; MITOCARRIER.
TE; PS00215; MITOCH CARRIER; 2.
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mitochondrial precursor
cleotide translocator 1)
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EMBL; X15711; CAA33742.1; -
EMBL; X152842; CAA26600.1; -
PIR; S14876; S14876.
MaizeDB; 17145; -
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SEQUENCE
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InterPro; IPR001993; Mitoch carri
Pfam; PF00153; Mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
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RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Horney T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
A Holroyd S., Horney T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones H., Jones M., Leather S., McDonald S., McLean J.,
RA Oliver K., O'Nell S., Pearson D., Quall M.A., Rabbinowitsch E.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Pearson D., Quall M.A., Rabbinowitsch E.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabbel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenz J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Gegnome sequence of Schizosaccharomyces pombe.",
RT "The genome sequence of Schizosaccharomyces pombe.",
RT "The genome sequence of Schizosaccharomyces pombe.",
RC --- SUBCNIT: Homodimer (By similarity).
CC --- SUBCNIT: Homodimer (By similarity).
CC --- SUBCNITINIAN LOCATION: Integral membrane protein. Mitochondrial
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01-NOV-1997 (Rel. 35, I
28-FEB-2003 (Rel. 41, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewar
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
   modified
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NCBI_TaxID=4896;
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                                                                                                                                                                                                          DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier family.
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   non-profit institutions as long and this statement is not removed.
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                                                                                                                                                                                                                                                                           SEQUENCE
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InterPro; IPR001993; Mitoch_carrier.
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                                                                                                      GATSLCFVYPLDFARTRLAAD---VGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV
                                                                                                                                                      EQGPLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAA 123
                     QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGWGGAFVLVLYDEIK 294
                                              VGIVVYRGLYFGMYDTLKPVVLVGPLEGNFLASFLLGWAVTTGSGVASYPLDTIRRMMM
                                                               QGIIIYRAAYFGVYDTAKG-MLEDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRWMM
                                                                                         GAASLLFVYSLDYARTRLANDAKSAKKGGERQFNGLVDVYRKTYRSDGLRGLYRGFGPSV
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Search completed: December 18, 2003, 12:41:23 Job time : 9.31467 secs

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Result
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PRINTS; PRO0926; MITOCARRIER.
PRINTS; PRO0784; MITOCHLING.
PROSITE; PS00215; MITOCH_CARRIER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Membrane; Transmembrane; Transport.
Membrane; Transmembrane; Transport.
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046373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           skeletal muscle.";
J. Biochem. 335:541-547(1998).
-i- SIMILARITY: BELONGS TO THE MITOCHONDRIAL EMBL; AB009386; BAA23777.1; -.
InterPro; IPR001993; Mitoch carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002067; Mit_uncoupling.
InterPro; IPR00230; Mit_uncoupling.
InterPro; IPR00230; Mit_uncoupling.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1993 (TrEMBLrel. 23, Last annotation update)
ADP/ATP translocase.
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"Identification of a 30kDa calsequestrin-binding protein, which
regulates calcium release from sarcoplasmic reticulum of rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
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                                         1 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                                                                                      Similarity
MSDQALSFLKDFLAGGVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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                                                                                                                                                        Score 1464.5; DB 6; Length Pred. No. 7.2e-129; 7; Mismatches 8; Indels
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01-JUN-2002
01-JUN-2002
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Q8BVI9;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The
                                                                                                                                                                                                                                                                                                                                                                                              the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK078077; BAC37117.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, Solute carrier family 25.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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                                                                                               QSGRKGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                                                                              QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                                                                                                             VQGIIIYRAAYEGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMM
                                                                                                                                                             VQGIIIYRAAYFGVYDTAKGMLDDFKNVHIFVSWMIAQSVTAVAGILLSYPFDTVRRRMM 239
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Query Match Best Local Similarity Matches 263; Conserv

Conservative

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Score 1392.5; DB 13 Pred. No. 4e-122; .8; Mismatches 16;

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SEQUENCE FROM N.A.

Yamazaki N., Shinohara Y., Tanida K., Ter

"Structural properties of mammalian mitoc
identification of possible amino acids th
differences in its isoforms.";
Mitochondrion 1:371-379(2002).

EMBL; AB065433; BAB84673.1; -.

InterPro; IPR001993; Mitoch_carrier.

Pfam; PF00153; mito_carr; 3.

PROSITE; PS900215; MITOCH CARRIER; 3.

SEQUENCE 298 AA; 32955 MW; CB6897BB98
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Q8AYM3;
01-MAR-2003 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
SEQUENCE FROM N.A.
Sato S., Seki Y., Sato K., Akiba
Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba
"Cold-induced mitochondrial uncoupling and expression of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color 
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
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Pred. No. 6.6e-124;
l6; Mismatches 13;
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MEDLINES-9003129; PubMed=9866197;

X Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

"The origin and differentiation of the heteromorphic sex chro
T. Z, W, X, and Y in the frog Rana rugosa, inferred from the seq
T a sex-linked gene, ADP/ATP translocase.";

L Mol. Biol. Evol. 15:1612-1619(1998).

C: --- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER PAMILY.

REMBL, AB008457; BAA36507.1; ---

REMBL, AB008457; BAA36507.1; ---

RINterPro; IPR001993; Mitoch_carrier.

InterPro; IPR002030; Mit_uncoupling.

Pfam; PF00153; mito_carr; 3.

Pfam; PF00153; mito_carr; 3.

PFINTS; PR00784; MTTOCHERRIER.

REPRINTS; PR00784; MTTOCH CARRIER; 3.

Membrane; Transmembrane; Transport.

SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;
                                                                                                                                                                                                                    Matches
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Best Local
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Q9YIC4;
01-MAY-1999
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                       VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIFISWMIAQSVTAVAGFASYPFDTVRRRMM
                                    VQGIIIYRAAYFGVYDTAKGMLFDDFKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM 239
                                                                                                                                                                 MTDAAISFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIMDCVVR
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                                                                                                                    88.7%; Score 1377.5; DE
86.6%; Pred. No. 1e-120;
Live 23; Mismatches 1
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Last annotation update)
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Ranidae; Rana
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Solute carrier family 25 member 5 protein.
SLC25A5.
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EMBL; AB008465; BAA36506.1; -
EMBL; AB008461; BAA36512.1; -
EMBL; AB008461; BAA36512.1; -
EMBL; AB008462; BAA36512.1; -
EMBL; AB008462; BAA36512.1; -
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR007926; MITOCARRIER.
PRINTS; PR007984; MTUNCOUPLING.
PROSITE; PS00215, MITOCH_CARRIER; 3.
Membrane; Transmembrane; Transport.
SEQUENCE 298 AA; 33054 MW; B0E23AD:
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MEDLINE=99083429; PubMed=9866197;

MIUTA I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

"The origin and differentiation of the heteromorphic sex chromosomes T. W., X., and Y in the frog Rana rugosa, inferred from the sequences of a sex-linked gene, ADP/ATP translocase.";

Mol. Biol. Evol. 15:1612-1619(1998).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
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01-MAY-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Pred. No. 1e-120; 
3; Mismatches 1
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Q9PRH2;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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EMBL; AF506216; AAM34660.1; -.
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Golling G., Amster
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
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Rana rugosa (Wrinkled frog).
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   AB008460; BAA36510.1; -. AB008458; BAA36508.1; -. AB008459; BAA36509.1; -.
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Last annotation update)
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InterPro; IPR002067; Mit_carrier.
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Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUTOCH_CARRIER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Membrane; Transmembrane; Transport
                                        InterFo; if into_carr; 3.

Pfam; PF00153; mito_carr; 3.

PRINTS; PR00926; mITOCARRIER.

PRINTS; PR00784; MTUNCOUPLING.

PROSITE; PS00215; MITOCH_CARRIER; 3.

PROSITE; PS00215; MITOCH_CARRIER; 3.

Membrane; Transmembrane; Transport.

Membrane; Transmembrane; Tyansport.
                                                                                                                     Crawford M.J., Khosrowshahlan F., Varmuza S.L., Liversag Txanopus Adenine Nucleotide Translocase mkNA Exhibits Sp Dynamic Patterns of Expression During Development."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.-I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAM EMBL; AF231347; AAF63471.1; -. EMBL; AF231347; AAF63471.1; -. InterPro; IPR001993; Mitoch Carrier. InterPro; IPR002067; Mit_carrier.
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Q919M9;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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NCBI_TaxID=8355;
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2003 (TrEMBLrel. 23, Las
nucleotide translocase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 AA;
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 Score 1366.5; DB 13
Pred. No. 1.1e-119;
3; Mismatches 17;
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Pred. No. 1.9e-120;
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Best Local S
Matches 236
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InterPro; IPR001993; Mitoch carrier.
InterPro; IPR002067; Mit carrier.
Pfam; PF00153; mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH CARRIER; 3.
SEQUENCE 299 AA; 33037 MW; 3C3BBCE
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Q95VX4;
01-DEC-2001
01-DEC-2001
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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80.3%; Pred. No. 2.3e-108;
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P SROUENCE FROM N.A.

P SROUENCE FROM N.A.

C STRAIN-SS mal seeking;

RT Chen Z., Fair J.A., Batterham P.;

RT A CDNA clone encoding the ADP/ATP translocase of Lucilia cuprina.";

RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

C: -: SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

DR EMBL; AP218587; AAF32322.1; -.

DR InterPro; IPR002067; Mitoch carrier.

DR InterPro; IPR002067; Mitoch carrier.

PFAm; PF00153; mitocarrier.

PFAm; PF00153; mitocarrier.

PRINTS; PR00926; MITOCARRIER; 3.

RRINTS; PR00926; MITOCARRIER; 3.

KW Membrane; Transmembrane; Transport.

CROHENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;
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RESULT

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Best Local 9
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SEQUENCE FROM N.A.

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MEDLINE=20196006; PubMed=10731132;

MEDLINE=20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.I.

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.I.

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang P., Pfeiffer B.
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01-MAR-2003
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Q8IRA0;
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01-OCT-2000
01-OCT-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Beoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Lucilia cuprina (Greenbottle fly)
Eukaryota, Metazoa, Arthropoda, H
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG16944-PC
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Calliphoridae; Lucilia.
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RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Gabor G.L., RA Abril J.F., Agbayani A., An H.J., Andrews-Frannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendaie J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Grerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA G. Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Posler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeywam C., RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., Laid Z., Liang Y., Lin X., Laid M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Melkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Melson D.R., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Shue B.C., Wassaman D.A., Weinstook G.M., Weinsenbach J., Wang X.H., Wang X.H., Wang X., Wang X.H., Wang X., Wang X.H., Wang X., Wang X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., RA Gibbs R.A., Wyer S., Wang A.H., Wang X., Smith H.O., Ra Gibbs R.A., Wareri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Smith H.O., Ra Gibbs R.A., Wareri J.S., Zhan M., Wang X., Zhu X., Smith H.O., Ra Gibbs R.A., Wareri J.S., Zhon M., Zhong G., Zhou X., Smith H.O., Ra Gibbs R.
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Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Conzalez M.; Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Gonzalez M.; Houck J., Hoskins R.A., Hostin D., Woshrefi A.,

Lbegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

AN Hilliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,

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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases EMBL; AE003484; AAN09267.1; -. SEQUENCE 312 AA; 34214 MW; 78D5834E74E168DF CRC64;
                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                           SEQUENCE FROM N.A.
Adams M.D., Celniker
Submitted (MAR-2000)
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e EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                             Venter C.J.;
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Query Match

79.98;

Score 1241;

DB 5;

Length 312;

QY 61 IPKEQGELSFWEGNLANVIRYEPTQALNEAFKDKYKQLELGGVDRHKQFWRYEAGNLAS
Qy 1 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
Query Match 79.5%; Score 1234.5; DB 13; Len Best Local Similarity 85.7%; Pred. No. 2.7e-107; Matches 233; Conservative 21; Mismatches 17; Indel
InterPro; IPR001993; Mitcoh_Carrier. DR InterPro; IPR002067; Mit_Carrier. DR Pfam; pF00153; mitco_carr; 3. DR PRINTS; PR00926; MITOCARRIER. DR PROSITE; P800215; MITOCH_CARRIER; 3. DR PROSITE; P800215; MITOCH_CARRIER; 3. KW Membrane; Transmembrane; Transport. SQ SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72 CRC
SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE-Liver; Cai Q., Storey K.B.; Cai Q., Storey K.B.; Submitted (APR-1999) to the EMBL/ -!- SIMILARITY: BELONGS TO THE MI EMBL; U44832; AAA57882.2;
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01-MAY-1999 (TrEMBLrel. 10, Last s 01-MAR-2003 (TrEMBLrel. 23, Last a ADP/ATP translocase. Rana sylvatica (Wood frog). Bukaryota; Metazoa; Chordata; Cran Amphibia; Batrachia; Anura; Neobat NCBI TaxID=45438;
SULT 13 1336 091336 PRELIMINARY; 091336; PRELIMINARY;
Qy 245 GADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKK
Qy 185 IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGILSYPFDTVRRRMMQSGRK
Qy 125 ATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII
Qy 65 QGELSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG
Qy 5 AWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKE : ::
Best Local Similarity 79.7%; Pred. No. 6.6e-108; Matches 232; Conservative 26; Mismatches 33;

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RESULT 15
044093
ID 04409
AC 04409
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DT ADDP/S
GN SESB
GO ENABRI
OC Neobat
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OC NOBI
RA Zeng
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  044093;
044093;
01-JUN-1998
01-JUN-1998
01-MAR-2003
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SEQUENCE
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InterPro; IPR001993; Mitoch carrier.
InterPro; IPR00167; Mit carrier.
Pfam; PF00153; mito carr; 3.
PRINTS; PR00926; MITOCARRIER; 3.
Membrane; Repeat; Transmembrane; Transport.
MON TER 288 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
Genetica 0:0-0(1997)
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER
EMBL; AF025799; AAB87884.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila subobscura (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP/ATP translocase (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG 124
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                                                                                                                                                                                                                                                                                                                           AMGFVKDFAAGGISAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMVDCFIRIPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 AA; 31775 MW; 06AlD1E477E81B26 CRC64;
  (Tremblrel. (Tremblrel. (Tremblrel. )
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(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                      PRELIMINARY;
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  23,
Created)
Last sequence update)
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Best Local
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InterPro; IPR001993; Mitoch carrier.
InterPro; IPR00167; Mit carrier.
Pfam; pF00153; mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Membrane; Repeat; Transmembrane; Transport.
NON_TER 288 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila pseudoobscura (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Bukoryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;

Bphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zeng L.-W., Comeron
Genetica 0:0-0(1997)
                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF025798; AAB87883.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP/ATP translocase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CBI_TaxID=7237;
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                                                  187
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246
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                                                                                                                                                                                                                       5 AWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKB
                                                                                                                                                                                                                                                                           Similarity
QGFLSFWRGNLANVIRYFFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASGGAAG
                                              ATSLCFVYPLDFARTRLAADTGKGGQREFTGLGNCLTKIFKSDGLVGLYRGFGVSVQGII
                                                                                                                             ATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSVQGII 184
                                                                                                                                                     QGFSSFWRGNLANVIRYFPTQALNFAFKDKYKQVFLGGVDKNTQFWRYFMGNLASGGAAG
                                                                                                                                                                                                        AIGFVKDFAAGGISAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMVDCFIRIPKE
                                                                         IYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMMQSGRK 244
                                                                                                                                                                                                                                                                                                                 288 AA;
                                                                                                                                                                                                                                                             Conservative .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Comeron J.M., Chen B., Kreitman M.;
                                                                                                                                                                                                                                                                                                               288
31725 MW; 052B0CC0050436B0 CRC64;
                                                                                                                                                                                                                                                                        76.2%;
79.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               THE MITOCHONDRIAL CARRIER FAMILY
                                                                                                                                                                                                                                                            Score 1183; DB 5;
Pred. No. 1.6e-102;
5; Mismatches 31;
                                                                                                                                                                                                                                                              31;
                                                                                                                                                                                                                                                                                     Length
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                       288
288
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Search completed: December 18, 2003, 12:43:09
Job time: 32.598 secs

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Title
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                       December 18, 2003, 12:34:56 ; Search time 35.3729 Seconds (without alignments) 1337.197 Million cell updates/sec
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Searched:	Scoring table: BLOSUM62 Gapop 10	Perfect score: 1547 Sequence: 1 MT
1107863 seqs, 158726573 residues	Gapop 10.0 , Gapext 0.5	US-U9-811-131-32 1547 1 MTDAALSFAKDFLAGGVAAALRGMGGAFVLVLYDEIKKYT 298

Minimum Maximum Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries 88 Beq length: length: 2000000000

Total number of hits satisfying chosen parameters:

1107863

										Database :	
10: /SIDS1/qcqdata/qeneseq/qeneseqp-embl/AA1989.DAT:*	: /SIDS1/g	8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*	7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT	6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT	5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*	4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*	3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*	2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*	1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*	A_Geneseq_19Jun03:*	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1454 1454	1454 1454 1454	1547 1537	1547 1547	Score
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AAU10380 AAM41427	AAY71033 AAM39641 AAU01200	AAU10379 AAO18516	AAY71032 AAU01199	ID
Human adenine nucl Human polypeptide	Human adenine nucl Human polypeptide Human adenine nucl	Human adenine nucl Human insulin rece	Human adenine nucl Human adenine nucl	Description

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ALIGNMENTS

AAY71032 standard; Protein; 298 B

AAY71032;

29-AUG-2000 (first entry)

Human adenine nucleotide translocator ANT2.

RESULT 1
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XX M Mi Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiparkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome. Homo sapiens.

WO200026370-A2

11-MAY-2000.

03-NOV-1998; 08-SEP-1999; 03-NOV-1999; 98US-0185904. 99US-0393441. 99WO-US25883.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or isgands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, cencephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MEDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 298
mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
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Ghosh SS;
                                                       Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
                                                                                              Human adenine nucleotide translocator-2 (ANT-2)
                                                                                                                                     07-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MITO-) MITOKOR
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                                                                                                                                                                                                            standard; Protein;
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                                                                                                                                                                                                                                                                                                                                              QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT 298
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llarity 100.0%;
Conservative 0
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                                                                                                                                   entry)
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Pred. No. 2.3e-154;
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                                                                                            protein.
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                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid expression constructs, useful for screening for authat alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule -
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
mitochondrial encephalopathy, lactic acidosis, stroke,
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Velicelebi G,
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241 QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDBIKKYT 298
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                                                                                                                                                                                                                                                                                                                MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLILQVQHASKQITADKQYKGIIDCVVR
                                                                                                             VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM 240
                                                                                                                                                                                                                                              IPKEQEVLSFWRGNIANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNIASG
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                                                                         VQGIIIYRAAYEGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLISYPEDTVRRRMM
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3, Davis RE;
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Pred. No. 2.3e-154;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC The invention relates to a recombinant expression construct (I) CC comprising a regulated promoter operably linked to a nucleic acid ce encoding an adenine nucleotide translocator (ANT) polypeptide. ANT CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT control mediate the exchange of ATP synthesised in the mitochondrial control matrix for ADP in the cytosol. (I) is useful for producing recombinant CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (I) is also useful for targeting a polypeptide of culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is CC expressed as a fusion protein with the polypeptide of interest. CC Recombinant ANT polypeptide, or cells expressing the polypeptide. ANT CC useful for identifying an agent that binds to an ANT polypeptide, concells expressing the polypeptide. CC preferably ANTI, ANT2 or ANT3 in a biological sample and for isolating CC ANT from a biological sample, where the ANT ligand is covalently or non-cc covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
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Ghosh SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 44; Fig 2; 147pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAY-2000; 2000US-0569327
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DB; AAS16689.
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GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                   GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                  I PKEQEVLS FWRGNLANVIR Y F PTQALNFA FKDKYKQI FLGGVDKRTQFWR Y FAGNLASG
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    Davis RB, Clevenger W, W
Moos WH, Pei Y, Carroll AK;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              identifying an agent that interacts with an ANT polypeptide. sequence represents the amino acid sequence of human ANT2.
                                                                                                                                                                                                                                                                                                                                                      Conservative
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DB; AAL48635.
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diabetes; metabolic syndrome;
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2001US-261456P.
2001US-261458P.
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2001US-261518P.
2001US-261531P.
2001US-261532P.
2001US-261532P.
2001US-261599P.
2001US-26159P.
2001US-261697P.
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The present invention relates to a method of identifying a candidate insulin receptor (INR) signaling modulating agent, involving contacting an assay system comprising an insulin receptor signaling modifier (ISM) polypeptide or nucleic acid with a test agent, and detecting a test agent-biased activity of the assay system. The method is useful for identifying candidate INR signaling modulating agents. ISM genes may be used as drug targets for treatment of disorders related to INR signaling

Identifying an insulin receptor signaling modulator, useful as drug targets for treating diabetes or metabolic disorders, comprises contacting an assay system comprising insulin receptor signaling modifiers with a test agent -

Disclosure;

Page 160-161; 232pp; English.

such as diabo

diabetes or metabolic syndrome. tides are useful for identifying

ISM nucleic acids and testing agents

that modulate

ISM function and for other applications related to the involvement of ISM in INR signaling, and for identifying subjects having a predisposition to such diseases associated with INR signaling. The present sequence is an ISM protein described in the exemplification of the invention.

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                                                                                                                                Anderson CM,
Ghosh SS;
                                                  WPI; 2000-365619/31.
N-PSDB; AAD00521.
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08-SEP-1999;
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2.6e-153;
les 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent discloses a method to produce adenine nucleotide translocator (C (ANT) proteins or ANT is a nuclear encoded protein and a major component of constructs. ANT is a nuclear encoded protein and a major component of constructs. ANT is a nuclear encoded protein and a major component of constructs are nitochondrial membrane. It mediates transport of adenosine (C di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents (C or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for (C existence) of the condrial pore activity, for treating diseases associated (C with altered mitochondrial function, including Alzheimer's, Parkinson's (C and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, (C encephalopathy, lactic acidosis and stropke (MELAS), hyperproliferative (C disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an accordance of the process of the condition of translocator ANT3 from human brain.
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 46; Page 173-174; 175pp; English
                                      241
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241
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QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
                                                                                  VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
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Pred. No. 1.4e-144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy;
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Recombinant construct encoding adenine nucleotide translocator

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Best Local :
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                      in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as Immune suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, hemotactic/chemokinetic activity, hemotactic/chemokinetic activity, darchemokinetic activity, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example
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19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunosuppressant
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                                                                                                                                                                                                                                                                                                                                                              .N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic, unosuppressant and cytostatic activity. The polynucleotides are useful
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DB; AAI58797.
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241
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                                                                                                                                                                                                                    1 MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
                                                                                                                                                                                                                                                                      Similarity
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Zhou
                                                                                                                          GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                               VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMM
                                                                                                GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                             I PKEQEVLS FWRGNLANVIRY FPTQALNFAFKDKYKQI FLGGVDKRTQFWRY FAGNLASG
QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
             QSGRKGTDIMYTGTLDCWRKJARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK 296
                                                VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                                   I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                     MTEQAISFAKDFLAGGIAAAISKTAVAPIBRVKLLLQVQHASKQIAADKQYKGIVDCIVR
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2000US-0598042.
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2000US-0653450.
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2000US-07273444.
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Wehrman T, X
Goodrich R,
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Xu C
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Pred. No. 1.4e-1
3; Mismatches
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Drmanac R
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e AJ,
RT;
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Yang
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Zhang J;
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RESULT 7
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression construct can alter mitochondrial membrane permeability translition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalogathy, lactic acidosis, stroke, because of the service                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents human adenine nucleotide translocator-3 (ANT-3) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MTP. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin; mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynuclectide encoding MPT polypeptide or cyclophilin polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murphy AN, C
Velicelebi G,
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                              GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                     I PKEQEVLS FWRGNLANVIRY F PTQALNFA FKDKYKQI FLGGVDKRTQFWRY FAGNLASG
  GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
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                                                                                                     I PKEQGVLS PWRGNLANVI RYFPTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
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3, Davis RB;
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                                                                                                                                                                                                                                                                                                            Score 1454; DB 22;
Pred. No. 1.4e-144;
3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e.g. cancer,
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                                                                                                                      comprising a regulated promoter operably linked to a nucleic acid comprising an adenine nucleotide translocator (ANT) polypeptide. ANT carbonism mediate the exchange of ANT synthesised in the mitochondrial matrix for ADF in the cytosol. (I) is useful for producing recombinant and polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. Crecombinant ANT polypeptide, or cells expressing the polypeptide. ANT cuseful for identifying an agent that binds to an ANT polypeptide, is cuseful for identifying an agent that binds to an ANT polypeptide, or referably ANT1, ANT2 or ANT3 in a biological sample and for isolating the present sequence of an ant polypeptide. Covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT3.
                                           Matches
                                                        Query Match
Best Local :
                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                Example
                                                                                                                                                                                                                                                                                                                                                                                                     Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human adenine nucleotide translocator 3
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                                                                                                                                                                                                                                                                                                                                                    invention relates to a recombinant
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1 MTDAALSFAKDFLAGGVAAAISKTAVAAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR 60
                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                             3; Fig 2; 147pp; English.
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                                           Conservative
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                                        Score 1454; DB 23;
Pred. No. 1.4e-144;
3; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                    expression construct (I) linked to a nucleic acid
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous

Novel nucleic acids and polypeptides, useful for such as central nervous system injuries -

treating

disorders

Example

2; SEQ ID NO 6358; 10078pp; English

system, such as peripheral

nervous injuries, peripheral

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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity -
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23-AUG-2000;
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                                    Anti; Adenine nucleotide translocator; cloning; screening; DNA Taq dideoxy terminator cycle sequencing; oxidative phosphorylation; probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy; hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy; lactic acidosis; degenerative muscle disease.
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Pred. No. 1.3e-140;
3; Mismatches 15;
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Query Match
Best Local S
Matches 265
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                                                                                      VQGIIIYRAAYFGIYDTAKGMLPDFKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
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                                                                    VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMM
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297
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AS X X X I D US 3

14-APR-2003 ABU53219;

(first

entry)

Human adenine nucleotide translocator ANT1

RESULT 12 ABU53219

ABU53219

standard;

Protein;

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RESULT 13
AAY71031
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DB Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention.
                                                            AAY71031;
                                                                                       AAY71031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids having the sequences of clones isolated from libraries different human tissues, useful in recombinant DNA methodologies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human metabolism-associated DKFZphtes3_35n12 homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example III; Page 850; 1095pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-327840/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wiemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-AUG-1999;
28-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; gene therapy; vaccine; disease treatment; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEHU-) GERMAN
                                                                                                                                                                                             245
                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                      185
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                                                                                                                                                                                                                                                                                                                125
                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                               264;
                                                                                                                                                                                                                                                                                                                                                                         65
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                            QEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAG 124
                                                                                                                                                                                                                                                                                                                                           QGFLSFWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASGGAAG
                                                                                         standard;
                                                                                                                                                                                 KGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                                                                                                                                            IIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMQSGR
                                                                                                                                                                                                                                                                                    ATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVSVQGI
                                                                                                                                                                                                                                                                                                     ATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGI
                                                                                                                                                                                                                         IIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMMQSGR
                                                                                                                                                                  KGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-IB01496
                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN GENOME PROJECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0149499
99US-0156503
                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15/
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1409; DB 22;
Pred. No. 7.7e-140;
5; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an adenine nucleotide translocator ANTI from human brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabstic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; alzheimer's disease; Parkinson's disease; Muntington's disease; dystonia; disbetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial disbetes and deafness; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson CM,
Ghosh SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; adenine nucleotide translocator; ANT1; mitochondria; ADP; ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent discloses a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 44; Page 172; 175pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MITO-) MITOKOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-365619/31.
DB; AAD00519.
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                                                           121 GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                    263;
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                                                                                                                                                                                                                                                IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120
GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,
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99US-0393441.
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                                                                                                                                                                                                                                                                                                                                                                                                           89.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   method to produce adenine nucleotide translocator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clevenger W,
                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                             Score 1391.5; DB 2:
Pred. No. 5.5e-138;
17; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wiley SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21; Length
                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                            297;
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Query Match Best Local Similarity

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Score 1391.5; DB 2 Pred. No. 5.5e-138;

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Sequence

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                                                 regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ERM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes miliothondrial encephalogathy, lactic acidesis, stroke, interaction of the preventia, mitochondrial encephalogathy, lactic acidesis, stroke,
                                                                                                                                                                                                                                                                                                             The present sequence represents human adenine nucleotide translocator-I (ANT-1) protein. ANT proteins are mitochondrial permeability translition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to with other mitochondrial core components e.g. cyclophilins to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin; mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-2000; 2000WO-US30535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human adenine nucleotide translocator-1 (ANT-1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-SEP-2001 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU01198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU01198 standard;
                                   hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murphy AN, C:
Velicelebi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200132876-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGWGGAFVLVLYDEIKKY 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQGIIIYRAAYFGIYDTAKGMLÞDÞKNTHIVISWMIAQTVTAVAGLTSYÞFDTVRRRMMM 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clevenger W,
G, Davis RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 2; 186pp; English.
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                                     disorders
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The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell an culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. Recombinant ANT polypeptide, or cells expressing the polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide. ANT polypeptide, is useful for determining the presence of an ANT polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 44; Fig 2; 147pp; English.
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N-PSDB; AAS16688.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; adenine nucleotide translocator; ANT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human adenine nucleotide translocator 1 (ANT1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-FEB-2002
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oos WH, Pei Y, Carroll AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                 ANT from a biological sample, where the ANT ligand is covalently or non-
covalently bound to a solid phase. Detectably labeled ANT ligand is also
useful for identifying an agent that interacts with an ANT polypeptide.
The present sequence represents the amino acid sequence of human ANT1.
                                                                                                                                                                                                                                                                                                                         Local Similarity
240
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                                                                                                                      121 GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
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                 QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDBIKKY 297
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QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                           VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM
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223 14.4 432 2 US-08-397-466-4 223 14.4 432 2 US-08-318-199-4 223 14.4 432 2 US-09-172-528-4 223 14.4 432 2 US-09-18-199-4 223 14.4 432 3 US-09-501-558-4 219.5 14.2 293 4 US-09-501-558-4 219.5 14.1 303 1 US-08-294-5228-36 217.5 14.1 303 1 US-08-218-8788-37 217.5 14.1 303 2 US-08-807-861A-37 217.5 14.1 303 2 US-08-470-868A-37 217.5 14.1 303 3 US-09-46-719A-37 217.5 14.1 303 3 US-09-910-68-37 217.5 14.1 303 3 US-09-946-719A-37 217.5 14.1 303 3 US-09-950-84-86-6 190.5 12.3 256 2 US-09-37-466-6 190.5 12.3 256 3 US-09-3718-199-6 190.5 12.3 256 3 US-09-503-579-6	23 14.4 432 2 US-09 23 14.4 432 2 US-09 23 14.4 432 2 US-09 23 14.4 432 3 US-09 23 14.1 303 1 US-09 25 14.1 303 1 US-08 25 14.1 303 2 US-08 25 14.1 303 3 US-08 25 14.1 303 3 US-08 25 14.1 303 3 US-08 25 12.3 328 3 US-08 25 12.3 328 3 US-08 25 12.3 328 3 US-08 25 12.3 328 3 US-08 25 12.3 328 3 US-08 25 12.3 328 3 US-09
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	-08-307-46-4 -08-37-466-4 -08-37-466-4 -09-3172-528-4 -09-3172-528-4 -09-3172-528-4 -09-503-579-4 -09-503-579-4 -09-501-558-4 -09-501-558-4 -08-278-36 -08-278-37 -08-807-861A-37 -08-807-861A-37 -08-807-861A-37 -08-946-719A-37 -08-946-719A-37 -08-946-719A-37 -08-946-719A-37 -08-946-719A-37 -08-946-719A-37 -08-946-719A-37 -08-946-719A-37 -09-317-528-6 -09-317-528-6 -09-318-199-6 -09-318-199-6 -09-318-199-6 -09-318-199-6 -09-318-199-6 -09-503-579-6

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/434,354; CURRENT FILING DATE: 1999-11-03; NUMBER OF SEQ ID NOS: 54; SOPTWARE: PASTSEQ for Windows Version 3.0; SEQ ID NO 48; LENGTH: 298; TYPE: PRT; ORGANISM: Homo sapien
US-09-434-354-48
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US-09-434-354-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 1547; DB 4; Best Local Similarity 100.0%; Pred. No. 1.2e-169;
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APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Prigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FO
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FO
TITLE OF INVENTION: DERTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
FILE REPERSNOE: 660088.433
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                       QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT 298
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                                                                                                      VQGIIIYRAAYFGIYDTAKGMLFDFKNTHIVISWMIAQTVTAVAGLTSYFFDTVRRRWMM 240
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RESULT 3
US-08-961-871-10
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                                                                                                                                                                                                                                Sequence 10, Application US/08961871
Patent No. 6013858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: MacGregor, Grant R.
APPLICANT: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
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APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Bileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigerl, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Velicelebi Gonul
APPLICANT: Davis, Robert E.
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GENERAL INFORMATION:
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SOFTWARE: FeatSEQ for Windows Version 3.0
SEQ ID NO 49
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
S-09-434-354-49
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                      CITY: Boulder
STATE: Colorad
COUNTRY: US
                                                               ZIP: 80303
                                                                                                                                                       STREET:
                                                                                                                                                                          ADDRESSEE:
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                                                                                      Colorado
Y: US
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                                                                                                                                                     E: Greenlee, Winner and Sullivan, 5370 Manhattan Circle, Suite 201
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                                                                                                                                                                                                                                                  RESULT 4
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APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert E.
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 265; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 91.2%;
Best Local Similarity 89.2%;
                                                                                                                                                                                  Sequence 47, Application US/09434354 Patent No. 6562563
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APPLICATION NUMBER: US/08/961,871
FILLING DATE: 31-OCT-1997
CLASSIFICATION INDEER: US 60/030,017
FILLING DATE: 31-OCT-1997
CLASSIFICATION ONTA:
APPLICATION NUMBER: US 60/030,017
FILLING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Perber; Donna M.
REFERENCE/DOCKET NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELEPHONE: (303) 499-8080
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (303) 499-808
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
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SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                              INFORMATION:
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; Pred. No. 5.6e-154;
15; Mismatches 17;
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERAFILE REFERENCE: 660088.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 47
LENGTH: 297

IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS

ORGANISM: Homo sapier

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FIITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C13
CURRENT PILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-23
PRIOR APPLICATION NUMBER: 60/06570
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1997-11-27
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
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US-09-996-243-289
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Grimaldi, J. Christopher
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Ferrara, Napoleone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                Daniel
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OR FILING DATE: 1998-06-09
OR APPLICATION NUMBER: 60/088734
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NUMBER: 60/089599

1998-06-17

APPLICATION NUMBER: 60/089801

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APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
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PRIOR TILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
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CURRENT APPLICATION NUMBER: US/09/188,930A
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PRIOR APPLICATION NUMBER: 60/091982
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APPLICATION NUMBER: 60/092182
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126 TSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGII 185 : | : | : | : | : | : | : | : | | 185
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                                                               GAKSLWRGNGINVLKIAPESAIKFMAYEOMKR--LVGSDQET---LRIHERLVAGSLAGA
                                                                                                      EVLSEWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QASIEGAPEVTMSSL--FKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIYPMEVLKTRMA--LRKTG---QYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAG
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                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          for Windows Version 3.0
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                                                                                                                                                                                                                                                     19.5%;
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29.1%; Pred. No. 5.4e-26;
                                                                                                                                                                                                                                    62;
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                                                                                                                                                                                                                                  Score 301; DB 3; I
Pred. No. 7e-26;
52; Mismatches 109;
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                                                                                                                                                                                                                                                                           DB 3; Length 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 469;
                                                                                                                                                                                                                                      Indels
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APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02

APPLICATION NUMBER: FILING DATE: 1998-07

NUMBER: 60/091519

1998-07-01

60/091544

FILING DATE: 1998-07-01 FILING DATE: 1998-06-26

APPLICATION NUMBER: 60/091360 APPLICATION NUMBER: 60/090863 APPLICATION NUMBER: 60/090862

APPLICATION NUMBER: 60/090696

LING DATE: 1998-06-25

FILING DATE:

1998-06-26

APPLICATION NUMBER: FILING DATE: 1998-06

LING DATE:

1998-06-25

APPLICATION NUMBER: 60/090695

1998-06-25

60/090694

LING DATE: 1998-06-25

PILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090690

APPLICATION NUMBER: 60/090678 APPLICATION NUMBER: 60/090676

LING DATE:

1998-06-25

APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24

APPLICATION NUMBER: 60/090542 APPLICATION NUMBER: 60/090540

LING DATE: LING DATE:

1998-06-24 1998-06-24 APPLICATION NUMBER:

ING DATE:

1998-06-24

60/090535

LING DATE:

1998-06-24

APPLICATION NUMBER: 60/090472

LING DATE: 1998-06-24

PLICATION NUMBER: 60/090445

APPLICATION NUMBER: 60/090435

1998-06-24 1998-06-24

ING DATE:

PLICATION NUMBER:

60/090444

LING DATE: 1998-06-24

APPLICATION NUMBER: 60/090429

LING DATE: 1998-06-23

LING DATE:

PPLICATION NUMBER: 60/090431

1998-06-24

APPLICATION NUMBER: 60/090349 APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090252

LING DATE: 1998-06-23

APPLICATION NUMBER:

60/090355

APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19

APPLICATION NUMBER: 60/089947 APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 APPLICATION NUMBER: 60/089600

LING DATE:

1998-06-18

LING DATE: 1998-06-19

APPLICATION NUMBER: 60/090246 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952

LING DATE:

1998-06-2

LING DATE: 1998-06-22

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RESULT 8
US-09-501-558-2
; Sequence 2, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:
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US-09-312-283C-339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from
TITLE OF INVENTION: and Methods for Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Watson, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 469
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                                                                                                                                                                                                                                                                                                                                                                                186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 TSLCFVYPLDFARTRLAADVGKAGAERBFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGII 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 GAKSLWRGNGINVLKIAPESAIKFMAYEOMKR--LVGSDQET----LRIHERLVAGSLAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 RHLVAGGGAGAVSRTCTAPLDRLKVLMQV-HASRSNNM------CIVGGFTQMIREG
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5. 6573095
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                                                                                                                                                                                                                                                                                                                                                                             IYRAAYFGIYDTAKGMLPDPKNTHI------VISWMIAQTVTAVAG-LTSYPFDT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGA 125
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                                                                                                                                                                 NLK 461
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                                                                                                                                                                                                                                                                                                                                   PYAGIDLAVYETL-----KNTWLQRYAVNSADPGVFVLLACGTISSTCGQLASYPLAL
                                                                                                                                                                                                                                                                                                                                                                                                                        IAOSSIYPMEVLKTRMA--LRKTG---QYSGMLDCARRILAKEGVAAFYKGYIPNMLGII
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Sleeman, Matthew
Onrust, Rene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62;
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                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,922
EARLIER PILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-482-273-118
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SOFTWARE: Fab
; SEQ ID NO 2
; STQTH: 291
                                                                                                                    SEQ ID NO 118
LENGTH: 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 118, Application US/09482273 Patent No. 6534631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Archur T.
APPLICANT: Sands, Archur T.
TITLE OF INVENTION: No. 6403784el Human Uncoupling Proteins
TITLE OF INVENTION: Polymucleotides Encoding the Same
FILE REFERENCE: LEX-0012-USA
CURRENT APPLICATION NUMBER: US/09/501,558
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 4
        TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (335)
                                                                                                                                                          EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: PZ030P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 LTAQRAAIVVGVELPVYDITKKHLILSGLMGDTVYTHFLSSF----TCGLAGALASNPVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 VSVQGIIIYRAAYFGIYDTAK-----GMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 CGILSGVISSTIANPTDVLKIRMQAQSNTIQG-----GMIGNFMNIYQQEGTRGLWKGVS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 SGGAAGATSLCFVYFLDFARTRLAADVGKAGABREFRGLGDCLVKIYKSDGIKGLYQGFN 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 AALSPAKDFLAGGVAAAISKTAVAPIBRVKLLLQVQHAS-----KQITADKQYKGIIDCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDEIKK 296
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Mathur, Brian
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27.8%; Pred. No. 4.3e-23;
tive 55; Mismatches 134;
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US-09-482-273-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KRIEF, STEPHANE
APPLICANT: BRIL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER APPLICATION NUMBER: EP 98401655.0
                                                                                                                                                                                                                                                                                                                                                                              Query Match 16.9%; Score 261.5; DB 4; Best Local Similarity 26.2%; Pred. No. 2.3e-21; Matches 77; Conservative 51; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e 4, Application US/09160119A
No. 6316219
INFORMATION:
                    245
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                                                                                                                                                                             129 CFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIYR 188
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                  KGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGG-AFVLVLYDEIKKY 297
                                                            AIYFPCYAHVKASFANEDGQVSPGSLLLA---GAIAGMPAASLVTPADVIKTR--LQVAA 324
                                                                                                   AAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTS----YPFDTVRRRMMQSGR
                                                                                                                                        IFTNPLEIVKIRLOV-----AGEITTGPRVSALSVVRDLGFFGIYKGAKACFLRDIPFS
                                                                                                                                                                                                                       RGLLPQLLGVAPEKAIKLTVNDFVRDKFMHKDGSVP-----LAAEILAGGCAGGSQV
                                                                                                                                                                                                                                                            RGNLANVIRYFPTQALNFAFKDKYKQIFL---GGVDKRTQFWRYFAGNLASGGAAGATSL 128
                                                                                                                                                                                                                                                                                                 FGLGSVAGAVGATAVY PIDLVKTRMQNQRSTGSFVGELMYKNSFDCFKKVLRYEGFFGLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMOSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDEIKK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIVVGVELPVYDITKKHLILSGMMGDTILTHFVSSF----TCGLAGALASNPVDVVRTRM 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGVLALYSGIAPALLRQASYGTIKIGIYQSLKRLFVERLEDET-----LLINMICGVVSG
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28.1%;
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Pred. No. 5.4e-23
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US-09-160-119-2
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LENGTH: 674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: EP 98401655.0 EARLIER FILING DATE: 1998-07-02 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KRIBF, STEPHANE APPLICANT: SOUCHBT, MICHEL APPLICANT: BRIL, ANTOINE
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552
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                                                                                                                                                                     443 IFTNPLEIVKIRLQV-----AGEITTGPRVSALSVVRDLGFFGIYKGAKACFLRDIPFS 496
                                                                                                                                                                                                             129 CFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIYR 188
                                                                                                                                                                                                                                                                                             72 RGNLANVIRYFFTQALNFAFKDKYKQIFL---GGVDKRTQFWRYFAGNLASGGAAGATSL 128
                                                                                                                                                                                                                                                                                                                                                                                 12 FLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKEQEVLSFW 71
RAGOTTYSGVIDCFRKILREEGPKALWKGAGARVFRSSPQFGVTLLTYELLQRW
                                                                                    AIYFPCYAHVKASFANEDGQVSPGSLLLA---GAIAGMPAASLVTPADVIKTR--LQVAA
                                     KGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNYLRGMGG-AFVLVLYDEIKKY 297
                                                                                                                         AAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTS----YPFDTVRRRMMQSGR
                                                                                                                                                                                                                                                     RGLLPQLLGVAPEKAIKLTVNDFVRDKFMHKDGSVP-----LAAEILAGGCAGGSQV 442
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ilarity 26.2%;
Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 261.5; DB 4;
Pred. No. 4.4e-21;
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RESULT 12
US-09-142-565-2
US-09-142-565-2
Sequence 2, Application US/09142565A
Patent No. 6187560
Patent No. 6187560
Patent No. 6187560
Patent No. 6187560
Patent No. 6187560
Patent No. 6187560
Patent No. 6187560
Patent No. 6187560
Patent Replicant James
PILICANT: Kelly Paine
APPLICANT: Robert James
PILICANT: ROBERT JAMES
PILE REFERENCE: GH-30002
PILE REFERENCE: GH-30002
PILE REPERENCE: GH-30002
PILE REPELICATION NUMBER: US/09/142,565A
CURRENT FILING DATE: 1997-03-05
EARLIER PILING DATE: 1997-03-18
EARLIER PILING DATE: 1997-03-18
EARLIER PILING DATE: 1997-03-18
EARLIER PILING DATE: 1997-07-16
NUMBER: OF SEQ ID NOS: 6
NUMBER: OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
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SEQ ID NO 2

ENGTH:

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RESULT 13
US-08-775-009-33
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
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APPLICANT: Gong, Weilong
APPLICANT: Emanuel, Beverly S.

APPLICANT: Budarf, Marcia L.

APPLICANT: New Bruce
TITLE OF INVENTION: Weliocardiofacial Syndrome Minimal Critical Region
TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: HOMO SAPIEN
                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CH-0681
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: 2009
APPLICATION NUMBER: US/08/775,009
FILING DATE: 27-DEC-1396
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: No. 5935783ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDVVKTRYM-----NSPPGQYFSPLDCMIKMVAQEGPTAFYKGFTPSFLRLGSWNVVMFV
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                                                           (215)
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                                                         568-3100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
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US-08-518-878B-51
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Tartag
                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,87/
FILLING DATE: 23-AUG-1995
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                                                                                                                                      TELEPHONE: (212) 790-9090
                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
              TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY:
                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
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                                                ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                            10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
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                                                 309 amino acids
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ilarity 28.1%;
Conservative (
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VENTION: COMPOSITIONS
VENTION: TREATMENT OF
                                                                                                                         (212) 869-9741/8864
unknown
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                single
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Pred. No. 1.2e-19;
7; Mismatches 138;
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BODY WEIGHT DISORDERS,
                                                                                                                                                                                                                                                                                                                      Version
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Length 309;

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RESULT 15
US-08-807-861A-51
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  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amin
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                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atent No. 5853975
GENERAL INFORMATION:
                                                                                                                NAME: COTUZZÍ, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tartaglia, ITLE OF INVENTION: MI
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 26 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASK---QITADKQYKGIIDCV 58
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5853975
amino acid
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                                                                                                 (212) 869-9741/8864
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26-FEB-1997
V: Ε11
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METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
                                                                                                                                                           7853-066
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nes 72; Conserv
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                                                                          237 VVKTRYMNSALGO-----YSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVT
                                                                                                             233 TVRRRMMOS-GRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLR-GMGGAFVLVL
                                                                                                                                                  181 PNVARNAIVNCABLVTYDLIKDALLKANLMTDDLPCHFTSAFGAGFCTTVIAS----PVD
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                                     YDBIKK 296
                                                                                                                                                                                     VSVQGIIIYRAAYFGIYDTAK-----GMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFD 232
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YEQLKR 296
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Search completed: December 18, 2003, 12:44:55 Job time : 13.3471 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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10 10 11 11 11 11 11 11	14 W W H	Result No.
1454 1454 1391.5 1391.5 1391.5 1391.5 741.5 741.5 741.5 741.5	1547 1547 1547 1454	Score
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Sequence 33, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 32501, A Sequence 7194, Ap Sequence 252, Appl Sequence 270, Appl Sequence 170, Appl Sequence 3338, Ap		Description

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ALIGNMENTS

120 120	Qy 61 IPKBQBVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG	
60	1 MTDAALSPAKDFLAGGVAAAISKTAVAPIBRVKLLLQVQHASKQITADKQXKGIIDCVVR	
60	Qy 1 MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR	
0,	Query Match 100.0%; Score 1547; DB 9; Length 298; Best Local Similarity 100.0%; Pred. No. 6.6e-159; Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps	
	; ORGANISM: Homo sapien US-09-811-094-32	
	; LENGTH: 298 ; TYPB: PRT	
	PastSEQ for	
	; CURRENT FILING DATE: 2001-03-14	
	; CURRENT APPLICATION NUMBER: US/09/811,094	
	NT LIGANDS AND SCREENING	
	; APPLICANT: Fe1, YAZDONG ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT);	
	: Ghosh,	
	•••	
	; APPLICANT: Wiley, Sandra Eileen	
	••	
	Davis, Robert E.	
	; APPLICANT: Anderson, Christen M.	
	; GENERAL INFORMATION:	
	· Datent No. U(S2001004414A)	
	05-09-811-094-32	
	RESULT 1	

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; Sequence 32, Application US/09185904A
; Patent No. USZ0020177185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
                                                                                          RESULT 3
US-09-185-904A-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REPERENCE: 66008 420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
S-09-810-644-32
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APPLICANT: Davis, Rob
APPLICANT: Clevenger,
APPLICANT: Willer, San
APPLICANT: Willer, Sc
APPLICANT: Szabo, Ton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3. Patent No.
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Best Local Similarity
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o. US20020012992A1
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Wiley, Sandra Eileen
Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Davis, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1547; DB 9; ilarity 100.0%; Pred. No. 6.6e-159; Conservative 0; Mismatches 0;
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; SOFTWARE: FastSEQ for I
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-185-904A-32
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Patent No. US20010044144A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiler, Scott W.
APPLICANT: Szabo, Tomas R.
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           TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 66008 4.42004
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
CURRENT FILING DATE: 33
COMPANDE OF SEQ ID NOS: 33
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APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomat R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
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TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 660088.420
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: Willer, Scott W.
: Szabo, Tomas R.
: Glosh, Soumitra S.
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Query Match Best Local Similarity

94.0%;

Score 1454; DB 9; Pred. No. 7.7e-149;

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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 33
LENGTH: 298:
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APPLICANT: Davis, Re
APPLICANT: Clevenge:
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CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
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ORGANISM: Homo sapien
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                   QSGRKGTDIMYTGTLDCWRKIARDEGGKAPFKGAWSNVLRGMGGAFVLVLYDEIKK 296
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Moos, Walter H.
Pei, Yazhong
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US-09-811-094-31
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; TYPE: PRT
; ORGANISM: Homo
US-09-185-904A-33
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APPLICANT: Anderson
APPLICANT: Davis, R
APPLICANT: Clevenge
APPLICANT: Wiley, S
APPLICANT: Willer,
APPLICANT: Szabo, T
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US-09-185-904A-33
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APPLICANT: Anderson, Christe
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, Willi
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APPLICANT: Wiley, Sandra Bileen
APPLICANT: Wiley, Sandra Bileen
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Sounitra S.
APPLICANT: Ghosh, Sounitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (AUTITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR CHERENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
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CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
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APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Sounttra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLECTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: THEREFOR
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Pred. No. 7.7e-149;
13; Mismatches 9;
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SEQ ID NO 31
LENGTH: 297
                                                                                                                                                                                 Query Match 89.9%; Score 1391.5; DB 9
Best Local Similarity 88.6%; Pred. No. 4.5e-142;
Matches 263; Conservative 17; Mismatches 16;
                                                                                                                                                                                                                                                                                                             SOPTWARE: FastSEQ for Windows Version SEQ ID NO 31
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                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL ANT LIGANDS AN FILE REFERENCE: 660088.420D3 CURRENT APPLICATION NUMBER: US/09/810,644 CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
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                                                                                                                                                                                                                                                               LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien
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ORGANISM: Homo sapien
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                                                                    IPKEQEVİSFWRĞNLANVIRYFPTQALNEAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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Clevenger, William
Wiley, Sandra Eileen
Willer, Scott W.
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Pred. No. 4.56
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RESULT 10
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-185-904A-31
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Sequence 32501, Application US/10029386
publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL, DAVID K.
APPLICANT: HOWAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GRITTE OF INVENTION: EXPRESSION ANALYSIS TWO
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Best Local Similarity
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Patent No. US20020177185A1
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CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
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Pred. No. 4.5e-142;
L7; Mismatches 16;
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REFERENCE: AEOMICA-X-2

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US-10-032-585-7194
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US-10-032-585-7194
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOPTWARE: PatentIn version 3.1
SEQ ID NO 7194
LENGTH: 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7194, Application US/10032585 Publication No. US20030180953A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 32501
LENGTH: 179
                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REPERENCE: 1018-205-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/029, CURRENT FILING DATE: 2001-12-20 NUMBER OF SEQ ID NOS: 34288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: MAP TO ACO04000.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.0

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.95

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96

OTHER INFORMATION: SWISSPROT HIT: P05141, EVALUE 2.00e-83
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 54.3%;
Local Similarity 98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 GDCLVKIYKSDGIKGLYQGFNVSVQGIIIYRAAYFGIYDTAKG 200
                                        117
  178
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                                                                                                                          59
                                                                                                                                                                                                                                                                                         163; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161;
                                                                                                                                                                 60
                                                                                                                                                                                                     Similarity
                                                                       GGAAGATSLCFVYPLDFARTRLAADV--GKAGAEREFRGLGDCLVKIYKSDGIKGLYQGF 177
                                                                                                                        RTAADEGVVSFWRGNTANVIRYPPTQALNFAFKDKFKAMF--GFKKDENYWKWFAGNLAS 116
                                                                                                                                                    RIPKEQEVLSFWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLAS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFLGGVDKRTQFWLYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFLGGVDKRTQFWRYFAGNLASGGAAGATSLCFVYFLDFARTRLAADVGKAGAEREFRGL 157
                                        GGLAGATSLAFVYSLDYARTRLANDAKSSKGDGKREFNGLVDVYKKTLASDGIAGLYRGF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDCLVKIYKSDGIKGLYQGFNVSVQGIIIYRAAYFGIYDTAKG
NVSVQGIIIYRAAYFGIYDTAKG-MLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRR 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQHASKQITADKQYKGIIDCVVRIPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                        50.4%;
                                                                                                                                                                                                                                                                                     ; Score 779.5; DB; Pred. No. 8e-76; 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 840; DB 12;
Pred. No. 1.1e-82;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                DB 12; Length 301;
                                                                                                                                                                                                                                                                                         84;
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RESULT 12
US-09-801-368-252
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RESULT 13
US-10-141-478A-2
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US-09-801-368-252
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LENGTH: 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 48.6%;
Best Local Similarity 54.3%;
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 199272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PATENTIA Version 3.0
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                                                                                                                                                                                                   184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159;
                                                                                                                                                                                                                                                                                                                                                 66 EVLSFWRGNLANVIRYFFTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                                                                                                                                                                                                                                22 NFLIDFLMGGVSAAVAKTAASPIERVKLLIQNQDEMLKQGTLDRKYAGILDCFKRTATQE 81
                                                                                                                                                                                                                                                                                                                      82 GVISFWRGNTANVIRYFPTQALNFAFKDKIKAMF--GFKKBEGYAKWFAGNLASGGAAGA 139
                                                                                                                                                                                                                                                                                                                                                                                                                         7 SFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQ-HASKQITADKQYKGIIDCVVRIPKEQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holtzman, Doug
Madden, Kevin
Maxon, Mary
Milne, Todd
No. US20020128250Alman,
                                                                                                                                                                                         IIIYRAAYFGIYDTAKG-MLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMMQS
                                                                                                                                                                                                                                                                         TSLCFVYPLDFARTRLAAD--VGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RYMMYTSGQA---VKYDGALDCERKVVAAEGVGSLEKGCGANILRGVAGAGVISLYDQLQ 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIK 295
                                                                                                                                                            IVVYRGLYFGMYDSLKPLLLTGSLEGSFLASFLLGWVVTTGASTCSYPLDTVRRRMMTS
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Sherman, Amir
Silva, Jeff
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                                                                                GQA---VKYDGAFDCLRKIVAAEGVGSLFKGCGANILRGVAGAGVISMYDQLQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Royer, John
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Hecht, Peter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 752.5; DB 10; Length 318; pred. No. 7.2e-73; 40; Mismatches 85; Indels 9;
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Sequence 2, Application US/10141478A Publication No. US20030148300A1 GENERAL INFORMATION:
APPLICANT: Valentin, Henry

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 47.9%;
Best Local Similarity 53.6%;
Matches 165; Conservative
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                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                TITLE OF INVENTION: Moss genes from Physcomitrella patens TITLE OF INVENTION: In the synthesis of carbohydrates FILE REFERENCE: BASF-NAE-1332-99-US CURRENT APPLICATION NUMBER: US/09/734,569 CURRENT FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 60/171,101
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APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/141,478A
CURRENT FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: US 60/289,519
PRIOR PILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/289,527
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: To Be Assigned, Attorney Docket No. US20030148300A1: 16517
PRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 1999-12-16
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SOFTWARE: PatentIn version 3.0
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APPLICANT: Zang, Wei
APPLICANT: Zang, Wei
TITLE OF INVENTION: Metabolite Transporters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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TYPE: PRT
ORGANISM: Arabidopsis thaliana
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196 GASSLLFVYSLDYARTRLANDAKAAKKGGGGRQFDGLVDVYRKTLKTDGIAGLYRGFNIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 EQEVLSFWRGNIANVIRYFFTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNIASGGAA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVGIIVYRGLYFGLYDSVKPVLLTGDLQDSFFASFALGWVI----TNGAGLASYPIDTVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----KKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRMMMQSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDBI-
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                                                                                                                                 Duwenig, Elke
Schmidt, Ralf-Michael
Reski, Ralf
                                                                                                                                                                                          Freund, Annette
                                                                                                                                                                                                                Frank, Markus
                                                                                                                                                                                                                                   Bischoff, Friedrich
                                                                                                                                                                                                                                                                                           Ehrhardt, Thomas
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Voelker, Toni
                                                                                                                                                                                                                                                                                                                                  Jens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297
                                                                                                                                                                                                                                                       Petra
                                                                                                                                                                                                                                                                         Andreas
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; Pred. No. 1.4e-71;
38; Mismatches 78;
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Matches

7 SFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITA---DKQYKGIIDCVVRIPK 63

Indels

12;

Gaps

Local

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                                                                                   ; ORGANISM: Aspergillus fumigatus US-10-128-714-3338
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US-10-128-714-3338
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 170
LENGTH: 386
TYPE: PRT
                                                                                                                                                                      SOFTWARE: PatentIn version 3.1 SEQ ID NO 3338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 47.9%;
Best Local Similarity 53.4%;
                                        Query Match
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                                                                                                                           LENGTH: 308
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jiang, Bo
APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lendeux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus
FILE REFERENCE: 10182-018-999
                                                                                                                                                                                                                PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/295,890 PRIOR FILING DATE: 2001-06-05 PRIOR APPLICATION NUMBER: US 60/303,899 PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/316,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242
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                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIIIYRAAYFGIYDTAKG-MLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMQ
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47.4%; Score 734; DB 15; 53.2%; Pred. No. 6.9e-71; ive 41; Mismatches 85;
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Pred. No. 1.5e-71;
12; Mismatches 86;
                                          Length 308;
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Search Job ti	皮	Ą	윩	Ą	Db	ş	Ф	Ş	F
Search completed: December 18, 2003, 12:55:43 Job time : 24.3606 secs	Db 244 TSGEAVKYKSSLDAARQIIAKEGVKSLFKGAGANILRGVAGAGVLSIYDQVQ 295		Db 184 LGIVVYRGLYFGMYDSIKPVVLVGSLEGSFLASFLLGWTVTTGAGIASYPLDTIRRRMMM 243		Db 124 GATSLLFVYSLDYARTRLANDAKSAKGGGERQFNGLIDVYRKTLASDGIAGLYRGFGPSV 183		Db 65 AEGVMSLWRGNTANVIRYFPTQALNFAFRDTYKSMFAYKKD-RDGYAKWMMGNLASGGAA 123		Db 7 AFTDSFAVGGVSAAVSKTAAAPIERIKLLVQNQDEMIRAGRLDRKYNGIIDCFRRTAQ 64
	295	295	RMMM 243	RMMM 240	3PSV 183	NVSV 181	3GAA 123	3GAA 123	RTAQ 64
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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(cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/paa/US06_COMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

4	Result No.
1547	Score
100.0	Query
298	Query Score Match Length DB ID
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1 1547 100.0 298 1 PCT-US01-15416-32 Sequence 32, Appl	ID
Sequence 32, Appl	Description

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ALIGNMENTS

; SEQ ID NO 32 ; LENGTH: 298 ; TYPE: PRT ; ORGANISM: Homo sapien	; CURRENT FILING DATE: 20; NUMBER OF SEQ ID NOS: 48; SOFTWARE: FABLSEQ for Wil	<pre>; TITLE OF INVENTION: THEREFO ; FILE REFERENCE: 660088.443PC ; CURRENT APPLICATION NUMBER:</pre>	; TITLE OF INVENTION:	•• ••		; APPLICANT: Dav. ; APPLICANT: Cle	<pre>; APPLICANT: MitoKor ; APPLICANT: Anders</pre>	; Sequence 32, Applica ; GENERAL INFORMATION:	RESULT 1
sapien	CURRENT FILING DATE: 2001-05-11 NUMBER OF SEQ ID NOS: 48 SOFTWARE: FastSEQ for Windows Version 3.0	TITLE OF INVENTION: THEREFOR FILE REFERENCE: 660088.443PC CURRENT APPLICATION NUMBER: PCT/US01/15416	10	Szabo, Tomas R. Ghosh, Soumitra S.	Wiley, Sandra Eileen Willer, Scott W.	Davis, Robert E. Clevenger, William	itoKor Anderson, Christen M.	Sequence 32, Application PC/TUS0115416 GENERAL INFORMATION:	
	. 0	416	RODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS						
			SCREENING ASSAYS						

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; SOFTWARE: FastSEQ for P
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
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US-09-185-904A-32
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CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
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 QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT 298
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Clevenger, William
                                                                                                                                                                                                                                                                        Conservative
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1: PRODUCTION OF ADENINE NUCLEOTIDE

1: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scott W.
                                                                                                                                                                                                                                                                                     100.0%;
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Pred. No. 2.9e-159;
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Pred. No. 2.9e-159;
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; ORGANISM: Homo sapien
US-09-393-441-32
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US-09-393-441-32
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SOFTWARE: Fabr
SEQ ID NO 32
FRIGTH: 298
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GENERAL I
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Best Local Similarity
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FO
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
FILE REFERENCE: 660088.433C1
CURRENT EPILICATION NUMBER: US/09/709,785
CURRENT FILLING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 57
                                                                                                                                                                      APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander '
APPLICANT: Frigeri, Luciano G.
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CURRENT APPLICATION NUMBER: US/09/393,441
CURRENT FILING DATE: 1999-09-08
NUMBER OF SEQ ID NOS: 37
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
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Pei, Yazhong
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ilarity 100.0%;
Conservative 0
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Pred. No. 2.9e-159;
Mismatches 0;
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TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRA
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASS
FILE REFERENCE: 660088.420D6
CURRENT APPLICATION NUMBER: US/09/809,827
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-809-827-32
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; ORGANISM: Homo
US-09-709-785-48
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LENGTH: 298
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APPLICANT: Davis, R
APPLICANT: Clevenge
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                                                                                                                                                                                                             Similarity
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                      GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
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                                                                                 IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120
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                                                              I PKEQEVLS FWRGNLANV I RYFPTQALNFAFKDKYKQ I FLGGVDKRTQFWRYFAGNLASG
                                                                                                                           MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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Pei, Yazhong
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                                                                                                                                                                                        100.0%; Silarity 100.0%; For Conservative 0;
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                                                                                                                                                                                          Score 1547; DB 23;
Pred. No. 2.9e-159;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1547; DB 21;
Pred. No. 2.9e-159;
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RESULT 7 US-09-810-644-32

Sequence 32, Application US/09810644 GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Bileen
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.

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US-09-809-889-32
; Sequence 32, Ap
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CURRENT APPLICATION NUMBER: US/09/809,889
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PastSEQ for Windows Version 3.0
SECULD NO 32
SECULD NO 32
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapien
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241
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Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
                                                                                                    VQGIIIYRAAYFGIYDTAKGMLFDFKNTHIVISWMIAQTVTAVAGLITSYFFDTVRRRMM 240
                                                                                                                                                                                        GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
                                                                                                                                                                                                                                                               IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120
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QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT
                                 QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT 298
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                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1547; DB 23; 100.0%; Pred. No. 2.9e-159; ative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOPTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 32
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-811-094-32
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-32
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; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
1.ENGENT: ???
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                                                                  Matches 298;
                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING FILE REFERENCE: 660088.420D4
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
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                       MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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   MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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                                                              100.0%;
ilarity 100.0%;
Conservative 0
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                                                                  Score 1547; DB 23;
Pred. No. 2.9e-159;
Mismatches 0;
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TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D5
CURRENT APPLICATION NUMBER: US/09/811,132
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-811-132-32
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Local Similarity 100.0%;
les 298; Conservative 0
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Wiley, Sandra Bileen
Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
                                                                                          VQGIIIYRAAYFGIYDTAKGMLÞDÞKNTHIVISWMIAQTVTAVAGLTSYÞFDTVRRRMM 240
                                                                                                                                               GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                     GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
                     QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAMSNVLRGMGGAFVLVLYDEIKKYT 298
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QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT
                                                                       VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
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Pred. No. 2.9e-159;
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RESULT 10 PCT-US02-01048-54

Sequence 54, Application PC/TUS0201048
GENERAL INFORMATION:
APPLICANT: EXLIXIS, INC.

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US-09-569-327-5
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APPLICANT: Davis, Ro
APPLICANT: Clevenger
APPLICANT: Wiley, Sa
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                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                   SEQ ID NO 5
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CURRENT FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2002-01-11
Prior Application removed - See File Wrapper
NUMBER OF SEQ ID NOS: 76
                                                                                                                                                                                                                                                            TITLE OF INVENTION: PRODUCTION OF ADEXINE NUCLEOTIDE TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS TITLE OF INVENTION: AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088.443
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                                                                                                                                   LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapiens
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Similarity 99.3%;
96; Conservative
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MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR 60
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Carroll, Amy K.
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Miller, Scott W.
Szabo Tomas R.
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                                                                         99.4%;
                                                           Score 1537; DB 19;
Pred. No. 3.5e-158;
1; Mismatches 1;
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Pred. No. 3.5e-158;
1; Mismatches 1;
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; ORGANISM: Homo sapiens
US-10-466-162-54
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US-10-466-162-54
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PRIOR FILING DATE: 2001-01-12
PRIOR PELICATION NUMBER: US 60/261,361
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,531
PRIOR PILING DATE: 2001-01-12
PRIOR PELICATION NUMBER: US 60/261,457
PRIOR APPLICATION NUMBER: US 60/261,226
PRIOR APPLICATION NUMBER: US 60/261,226
PRIOR APPLICATION NUMBER: US 60/261,226
PRIOR APPLICATION NUMBER: US 60/261,304
PRIOR APPLICATION NUMBER: US 60/261,304
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PRIOR APPLICATION NUMBER: US 60/261,304
PRIOR PILING DATE: 2001-01-12
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LENGTH: 298
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Best Local Similarity
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CURRENT FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: US 60/261,335
PRIOR FILING DATE: 2001-01-12
PRIOR PRIOR PRIOR DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
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TITLE OF INVENTION: Modulating Insulin Receptor Signaling
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                                        GAAGATSLCFVYPLDFARTRLAADVGKAGAERBFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
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GÄAGATSLCFVYPLDFARTRLÄÄDVGKÄGÄEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
                                                                                                IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120
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                                                                                                                                                 IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120
                                                                                                                                                                                                    MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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Pred. No. 3.5e-158;
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181

VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM 240

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US-09-760-469-1767
Sequence 1767, Application US/09760469
SERERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ54
CURRENT APPLICATION NUMBER: US/09/760,469
CURRENT FILING DATE: 2001-01-16
CURRENT FILING DATE: 2001-01-16
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                                                                                                                       Prior application data removed -
NUMBER OF SEQ ID NOS: 1983
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1767
LENGTH: 332
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SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20286
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APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION FILE REFERENCE: CL001450
CURRENT APPLICATION NUMBER: US/60/452,680
CURRENT FILING DATE: 2003-03-07
                                                                      TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
LOCATION: (8)
OTHER INFORMATION:
NAME/KEY: SITE
                                                      NAME/KEY:
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TYPE: PRT
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                                                          SITE
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                  Xaa equals
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Pred. No. 3.5e-158;
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                 of the naturally occurring
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US-10-216-583-1767
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Best Local S
Matches 296
                                 Sequence 1767, Appli GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 296; Conserv
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                                                                                                                                                                                                                                                                                            GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
                                                                                                                                                         QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT 298
                                                                                                                                                                                                                                                                                                                                              IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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                                                                                                                                       QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT 332
                                                                                                                                                                                                       VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
                                                 Application US/10216583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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   and
 Antibodies
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CURRENT APPLICATION NUMBER: US/10/216,583
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/760,469
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR PILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR PILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR APPLICATION NUMBER: 60/218,290
                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 1983
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1767
LENGTH: 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-07-14
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                                                                                                                    LOCATION: (8) OTHER INFORMATION: Xaa
                                                                                                                                                                      PEATURE: misc_feature
                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                              FEATURE
NTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                               NAME/KEY: misc_feature
                                                                                                                       equals
                                                                                                                       any of the naturally occurring L-amino
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Db	Q	망	Ş	문	Ş	B	8	В	Ş	Query Match Best Local : Matches 29	US-10-21
275 QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT 332	241 QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT 298	215 VQGIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMM 274	181 VQGIIIYRAAYPGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM 240	155 GAAGATSLCFVYPLDFARTRLAADVGKAGAERBFRGLGDCLVKIYKSDGIKGLYQGFNVS 214	121 GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180	95 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 154	61 IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG 120	35 MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR 94	1 MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR 60	Query Match 99.4%; Score 1537; DB 28; Length 332; Best Local Similarity 99.3%; Pred. No. 4.1e-158; Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	US-10-216-583-1767

Search completed: December 18, 2003, 12:53:25 Job time : 166.852 secs

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Run on: December 18, 2003, 12:37:46; Search time 14.3494 Seconds (without alignments) 1997.178 Million cell updates/sec

Title: Perfect score: US-09-811-131-32 1547

Scoring table: 1 MTDAALSFAKDFLAGGVAAA......LRGMGGAFVLVLYDEIKKYT 298

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 283308

283308 seqs, 96168682 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	. 15	14	13	12	11	10	9	80	7	9	5	4	ω	L	1	Result No.
746	749.5	749.5	752	752.5	753	754	757	759	759	761.5	765	770	771	938	968	986	1029	1029	1032	1170	1413	1417	1417	1419	1454	1458	1479	1547	Score
48.2	48.4	•	8	48.6	8	8	48.9	49.1	49.1	49.2	49.5	49.8	•	60.6	•	63.7	٠	66.5	•	•	91.3	91.6	91.6	91.7	•		95.6	100.0	Query Match
306	306	305	386	318	387	386	313	387	326	307	308	322	386	301	339	300	313	313	300	301	298	298	298	298	298	298	298	298	Length
2	N	N	N	_	N	N	_	N	N	N	<u>, , , , , , , , , , , , , , , , , , , </u>	N	N	N	N	N	N	N	N	<u>.</u>	_	N	N	H	μ	N	N	μ	B
T42011	T20012	S68154	S21974	A31978	S16568	S17917	XWNC	S14876	T25728	A36582	S30259	T40526	T09709	851132	A41677	T15206	T25850	T23207	T25371	S31935	A44778	I60173	837210	XWBO	S03894	B43646	S31814	A29132	ID
	tical pro	carrier	ADP, ATP carrier pr	carrier	ADP, ATP carrier pr	carrier	ADP, ATP carrier pr	carr	О	carrier	ATP	transloc	carrier	carrier	-		-		tical pro	carr	ADP, ATP carrier pr			carrier	carrier	,ATP carrier	ADP, ATP carrier pr	ADP, ATP carrier pr	Description

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181 VQGIIIYRAAYFGIYDTAKGMLPDPKVTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM 240

		356	39 372 10 372	388	521.5	665.5	728	741.5	741.5	745	745.5	746
21.6	22.0	23.0	24.0 24.0	25.1	33.7	13.0	47.1	17.9	17.9	18.2	48.2	18.2
348 2 332 2	358 2	352 2 475 2	381 2 415 2	325 2	327 2	298 2	309 2	386 2	379 2	382 2	385 1	379 2
D84798 T47703	T45934	T01729	T51158 T48171	T04273	T51577	T24029	A24849	S14874	821313	833630	S29852	T04608
probable mitochond Ca-dependent solut	hypothetical prote	mitochondrial solu	hypothetical prote hypothetical prote	hypothetical prote	ADP/ATP translocas	hypothetical prote	ADP, ATP carrier pr	ADP, ATP carrier pr	ADP, ATP carrier pr	ADP, ATP carrier pr	carrier	ADP, ATP carrier pr

ALIGNMENTS

 KGLYQGFNVS 180	b 121 GAAGATSLCEVYELDEAKTRLAADVGKAGAEREERGLGDCLVKIYKSDGIKGLYQGENVS	B 5
	61	. B &
OXKGIIDCVVR 60 QXKGIIDCVVR 60	y 1 mtdaalspakdplaggvaaaisktavapiervklllqvqhaskqitadkqykgiidcvvr 	B &
98; 0; Gaps 0;	Query Match 100.0%; Score 1547; DB 1; Length 298; Best Local Similarity 100.0%; Pred. No. 4e-130; Matches 298; Conservative 0; Mismatches 0; Indels 0	
ces for GDB:ANT2 and GDB: repeat homology e protein >	A;Gene: GDB:ANT2; T3; 2F1 A;Gene: GDB:ANT2; T3; 2F1 A;Gene: GDB:ANT2; T3; 2F1 A;Cross-references: GDB:125190; OMIM:300150 A;Cross-references: GDB:125190; OMIM:300150 A;Map position: Xq13-Xq26 A;Map position: Xq13-Xq26 A;Mabe: there may be some confusion in the assignment of sequences for C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein; transmembrane prote; Keywords: duplication; homodimer; mitochondrion; transmembrane prote; Keywords: duplication; homodimer; mrotein repeat homology <acp1> F;510-202/Domain: ADP,ATP carrier protein repeat homology <acp3> F;207-298/Domain: ADP,ATP carrier protein repeat homology <acp3></acp3></acp3></acp1>	444CCPPPP(
PID:g339721	NA G',67-110,'L',112-161,'G',163-298 <hou> GB.J03591; NID:g339720; PIDN:AAA36749.1; ce: clone pHAT3</hou>	7 P P P P
PID:g179247 essed at the mRNA level in a	J02683; NID:9179246; PIDN:AAA35579.1; rdi, G. U.S.A. 85, 377-381, 1988 enes for ADP/ATP translocase are expr 197; MUID:88124845; PMID:2829183	A A P R A
carrier which is growth-regulat	J. Biol. Chem. 262, 4355-4359, 1987 A;Title: Molecular cloning of a cDNA for a human ADP/ATP carrie: A;Reterence number: A29132; MUID:87166056; PMID:3031073 A;Accession: A29132 A;Molecule type: mRNA A;Residues: 1-298 <bat></bat>	*****
17-Mar-2000 , S.; Baserga, R.	carrier protein T2 - h ate names: mitochondri s: Homo sapiens (man) 17-Mar-2000 #sequence ion: A29132; C28116	RCCCN PAR

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A;Molecule type: mRNA
A;Residues: 1298 <POW>
A;Residues: 1298 <POW>
A;Residues: 1298 <POW>
A;Cross-references: GB:M24103; NID:g529416; PIDN:AAA30769.1; PID:g529417
A;Cross-references: GB:M24103; NID:g529416; PIDN:AAA30769.1; PID:g529417
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein formorior; transmembrane protein
C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology
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                                                                                                                                                         Biochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase
A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Accession: B43646
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                 RESULT 3
B43646
ADP.ATP carrier protein T2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Species: 13-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                              C;Accession: B43646
R;Powell, S.J.; Medd, S.M.; Runswick,
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F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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$31814
ADP,ATP carrier protein T2
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
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A; Residues: 1-298 < COS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIFISWMIAQSVTLVAGLTSYPFDTVRRRMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I PKEQEVLS FWRGNLANVIRY FPTQALNFA FKOKYKQI FLGGVDKRTQ FWRY FAGNLASG
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Pred. No. 4.5e-124;
                                                                                                                                                                                                                                                                                M.J.; Walker,
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A;Cross-references: GDB:125184; OMIM:300151; OMIM:403000
A;Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F;2-298/Product: ADP,ATP carrier protein #status predicted <MAT>
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP,ATP carrier protein T3 - human
N/Alternate names: ADP,ATP carrier protein T2
C/Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 36-104, R; 106, A', 109-298 <HOU>
A;Cross-references: GB:J03592; NID:g339722;
A;Experimental source: liver
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A;Title: DNA sequences of two expressed nuclear genes f
A;Reference number: S03893; MUID:89236396; PMID:2541251
A;Accession: S03894
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R;Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase are expressed at A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: B28116
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C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000
C;Accession: S03894; B28116
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                                                                                                                                                                   Matches 274;
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Best Local :
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                                                                                                                     1 MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
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                                                                                                                                                                                           Similarity
IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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                                                                                                                                                                     13; Mismatches
                                                                                                                                                                Score 1454; DB 1;
Pred. No. 7.6e-122;
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                                                                                                                                                                                                            Length 298;
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A;Accession: Asis:
A;Accession: Asis:
A;Molecule type: protein
A;Residues: 205-298 (ABAb)
A;Residues: 205-298 (ABAb)
R;Oettmeier, W.; Masson, K.; Kalinna, S.
Bur. J. Biochem. 227, 730-733, 1995
Bur. J. Biochem. 227, 730-733, 1995
A:Title: [(3)H]7-azido-4-isopropylacridone
A:Title: [(3)H]7-azido-9; MUID:95172058;
                          A;Description: catalyzes the exchange between cytosolic ADP and mitochondrial A;
A;Note: located in the inner mitochondrial membrane
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein; methylated amino acid,
C;Keywords: acetylated amino end; duplication; homodimer; methylated amino acid,
C;Seywords: ADP,ATP carrier protein repeat homology ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology ACP2>
C;207-298/Domain: ADP,ATP carrier protein repeat homology ACP3>
C;207-298/Domain: ADP,ATP carrier protein repeat homology ACP3>
C;207-298/Domain: ADP,ATP carrier protein repeat homology ACP3>
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C;207-298/Domain: ADP,ATP carrier protein repeat homology ACP3>
C;207-298/Domain: ADP,
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A; Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298
A; Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298
A; Note: residue 52 may be methyllysine
R; Babel, W.; Wachter, E.; Aquila, H.; Klingenberg,
Biochim. Biophys. Acta 670, 176-180, 1981
A; Title: Amino acid sequence determination of the J
A; Reference number: A61343; MUID: 82046808; PMID: 62:
A; Accession: A61343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 208-298 < RAS>
A; Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1;
A; Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1;
A; Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1;
A; Cross-references: CB:M13783; NID:g162630; PIDN:AAA30363.1;
A; Title: Complete amino acid sequence of the ADP/ATP carrier
A; Reference number: A03181; MUID:82188267; PMID:7076130
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N;Alternate names: ADP/ATP translocase T1
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence revision 22-Jul-1994 #text_change
C;Accession: A43646; A24822; A03181; A61343; S69369
C;Accession: A43646; A24822; A03181; A61343; S69369
R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Blochemistry 28, 866-873, 1989
Biochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase
A;Reference number: A43646; MUID:89229093; PMID:2540808
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A;Cross-references: GB.M24102; NID:g529414; PIDN:AAA30768.1; R;Rasmussen, U.B.; Wohlrab, H.
Biochem. Biophys. Res. Commun. 118, 850-857, 1986
A;Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two diac,Reference number: A24822; MUID:86295775; PMID:3017341
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 49-63; 154-168 < OET>
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R;Laplace, C.; Costet, P. submitted to the EMBL Data A;Reference number: S37210 A;Accession: S37210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein; Keywords: duplication; transmembrane protein protein; ADP,ATP carrier protein repeat homology <ACP1>;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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                                                                                   VQGIIIYRAAY FGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPPDTVRRRMM
                                                                                                                                                                                                                 GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
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                                          QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMM 240
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Pred. No. 1.5e-118;
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Pred. No. 16
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A/Status: not compared with conceptual A/Molecule type: DNA A/Residues: 1-298 <COZ>
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A;Cross-references: GB:J04982; NID:g178658; PIDN:AAA51736.1;
A;Cross-R. A.L.; Runswick, M.J.; Walker, J.E.
T. Mol. Biol. 206, 261-280, 1989
A;Title: DNA sequences of two expressed nuclear genes for hum A;Reference number: S03893; MUID:89236396; PMID:2541251
A;Accession: S03893
                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Title: A human muscle adenine nucleotide translocator gene has four exons, A,Reference number: A44778; MUID:89340499; PMID:2547778 A,Accession: A44778
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F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A;Residues: 1-298 <RES>
A;Cross-references: EMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Homo sapiens (man)
| Species: Homo sapiens (man)
| Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
| Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
| Accession: A44778; S03893; A39891; A28116
| Accession: A44778; S03893; A39891; A28116
| Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Li, K.; Warner, C.K.; Hodge, J.; Li, K.; Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, Warner, C.K.; Li, W
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;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
;Keywords: duplication; transmembrane protein
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Pred. No. 1.5e-118;
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R;Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C. Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A;Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: A;Reference number: A39891; MUID:88041149; PMID:2823266
A;Accession: A39891
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP,ATP carrier protein - African malaria mosquito (Species: Anopheles gambiae (African malaria mosquito) (Cjapecies: Anopheles gambiae (Prican malaria mosquito) (Cjapecies: Cjapecies: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; S31936 (Cjaccession: S31935; Cjaccession: S31935; S31936 (Cjaccession: S31935) (Cjaccession: S31935; S31936 (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession: S31935) (Cjaccession
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A;Title: Two distinct genes for ADP/ATP translocase are
A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: A28116
A;Cross-references: EMBL:Z21814; EMBL:Z21816;
C;Superfamily: ADP,ATP carrier protein; ADP,ATP
C;Keywords: duplication; transmembrane protein
E;7-101/Domain: ADP,ATP carrier protein repeat h
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G;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein E;2-298/Product: ADP,ATP carrier protein #status predicted <MAT> F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1> F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2> F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A; Residues: 1-15, /A; 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>
A; Cross-references: GB: J02966; NID: g339919; PIDN: AAA61223.1; P
A; Experimental source: clone pHMANT
R; Houldsworth, J.; Attardi, G.
                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <BEA>
                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, February 1993
A;Description: A cDNA encoding an ADP/ATP carrier
A;Reference number: S31935
A;Accession: S31935
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A;Residues: 1-37 <HOU>
A;Cross-references: GB:J03593; NID:g339724; PIDN:AAA36751.1;
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Pred. No. 3.4e-118;
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A; Map position: 3
A; Introns: 20/1; 41/3;
C; Superfamily: ADP, ATP
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A;Molecule type: DNA
A;Residues: 1-300 <WIL>
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T25371
T25371
T25371
hypothetical protein T27E9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: C5-Ct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C;Accession: T25371
R;Lloyd, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number:
A;Accession: T25371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, A;Reference number: Z20024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z82059; PIDN:CAB04874.1; GSPDB:GN00021;
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     Gene: CESP:T27E9.1
                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                     LSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGATS
                    TDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDBIKKY 297
                                                                                RAAYFGIYDTAKGML-PDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMQSGRKG
                                                                                                                                                                                    AALWRGNLANVIRYPPTQAMNFAPKDTYKAIFLEGLDKKKDFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIK 295
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                                                                                                                        LCFVYPLDFARTRLAADIGKAN-DREFKGLADCLIKIVKSDGPIGLYRGFFVSVQGIIIY
                                                                                                                                                                                                                                                FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASKAIAVDKRYKGIMDVLIRVPKEQGV
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   -DILYKNTLDCAKKIIQNEGMSAMFKGALSNVFRGTGGALVLAIYDBIQKF
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78.1%;
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                                                                                                                                                                                                                                                                                                         Score 1032; DB 2;
Pred. No. 2.9e-84;
4; Mismatches 50;
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Pred. No. 1.
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T25850
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                                                          A;Gene: CESP:T01B11.4
A;Map position: 4
A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP
                                                                                                                                                                                                                                           R;Geisel, C.; Stellyes, L. submitted to the EMBL Data Library, A;Description: The sequence of C. e.
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A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP
                                                                                                                        A; Experimental source: C; Genetics:
                                                                                                                                                                   A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-313 <GEI>
                                                                                                                                                                                                                    A; Accession:
                                                                                                                                                                                                                               A; Reference number: Z20099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated
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Best Local Similarity Matches 206; Conserv
                               Query Match
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Best Local :
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision
C;Accession: T25850
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A;Experimental source: clone K01H12
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                                                                                                                                                                                                            A;Cross-references: EMBL:U80931; PIDN:AAB38001.1; GSPDB:GN00022; A;Experimental source: strain Bristol N2; clone T01B11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T01B11.4 - Caenorhabditis elegans
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                                                                                           carrier protein; ADP, ATP carrier protein repeat
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                     66.5%; Score 1029; DB 2; 70.8%; Pred. No. 5.6e-84;
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; Pred. No. 5.6e-84;
28; Mismatches 53
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Mismatches
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                                        Length 313;
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ADP,ATP carrier protein - Chlorella kessleri
C;Species: Chlorella kessleri
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
                                                           RESULT 14
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
F;9-103/Domain: ADP,ATP carrier protein repeat homology <ACR>
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C;Accession: T15206
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A;Residues: 1-300 <LET>
A;Cross-references: EMBL:AF003141; NID:g2088732; PID:g2088738; PIDN:AAB54179.1; GSPDB:GN
A:Experimental source: strain Bristol N2; clone W02D3
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A; Accession: T15206
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Similarity 67.5%; Pred. No. 3.6e-80;
                                                                                                                                                                                                                                                                                                                                                                                                        LSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKEQEV
                                                                                                                                                                                  TDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIK 295
                                                                                                                                                                                                                        RAAYFGMFDTAKTLYSTDGQKLNFFTTWAIAQVGTVGSGYLSYPWDTVRRRMMQSGRK-
                                                                                                                                                                                                                                                             RAAYFGIYDTAKGML-PDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRWMQSGRKG
                                                                                                                                                                                                                                                                                                      LCFVYPLDFVRTRLGADVGK-GVDREFQGLTDCFVKIVKSDGPIGLYRGFFVSVQGIIIY
                                                                                                                                                                                                                                                                                                                                         LCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIY
                                                                                                                                                                                                                                                                                                                                                                                  AAFWRGNLANVLRYFPTQALNFAFKDTYKKMFQEGIDKNKEFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLVDLASGGTAAAISKTAVAPIERVKLLLQVSDVSETVTADKKYKGIMDVLARVPKEQGY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AALWRGNLANVIRYFPTQALNFAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSFWRGNLANVIRYFFTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGATS 127
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                                                                                                                                             -DILYKNTLDCVRKIVKNEGITALYKGGLSNVFRATGGALVLTIYDEIQ 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAAYFGIYDTAKGML-PDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMQSGRKG
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Conservative

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Indels

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Gaps

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60

RIPKEQEVLSFWRGNLANVIRYFPTQALNFAPKDKYKQIFLGGVDKRTQFWRYFAGNLAS 119

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A; Status: preliminary
A; Molecule type: mRNA
A; Medlecule type: mRNA
A; Residues: 1-33 < HIL>
A; Residues: 1-33 < HIL>
A; Cross-references: GB:M76669; NID:g516596; PIDN:AAA33027.1; PID:g516597
C; Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology exacens protein
C; Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F; 38-134/Domain: ADP, ATP carrier protein repeat homology <ACP1>
F; 144-235/Domain: ADP, ATP carrier protein repeat homology <ACP3>
F; 241-329/Domain: ADP, ATP carrier protein repeat homology <ACP3>
                                                                                          A;Molecule type: mRNA
A;Residues: 1-301 <-HAT
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A;Residues: 1-301 <-HAT
Carrier protein; ADP,ATP carrier protein
E;G-102/Domain: ADP,ATP carrier protein repeat homology <-ACP1>
E;112-203/Domain: ADP,ATP carrier protein repeat homology <-ACP2>
F;209-301/Domain: ADP,ATP carrier protein repeat homology <-ACP3>
                                                                                                                                                                                                                                                                                                                           C;Pate: 07-May-1995 #sequence revision 01-Sep-1995 #text_change 09-Jun-2000 C;Accession: S68993; S51132
C;Accession: S68993; S51132
R;Hatin, I.; Jaureguiberry, G.
Bur. J. Biochem. 228, 86-91, 1995
Bur. J. Biochem. 228, 86-91, 1995
A;Title: Molecular characterisation of the ADP/ATP-transporter cDNA from the A;Reference number: S68993; MUID:95188918; PMID:7883016
A;Accession: S68993
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S51132
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R;Hilgarth; C.; Sauer, N.; Tanner, W.
J. Biol. Chem. 266, 24044-24047, 1991

A;Title: Glucose increases the expression of the ATP/ADP translocator and A;Reference number: A41677; MUID:92084708; PMID:1748677

A;Accession: A41677
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                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: ADP/ATP transporter C;Species: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP,ATP carrier protein - malaria parasite (Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    닭
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 GRKGIDIMYIGILDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKY 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 MAFVKDILAGGTAGAISKTAVAPIERVKLILQTQDSNPMIKSGQVPRYTGIVNCFVRVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---GGERQYNGTIDCWRKVAQQEGMKAFFKGAWSNVLRGAGGAFVLVLYDEIKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIIYRAAYFGIYDTAKGML-PDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMMQS
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                         60.6%;
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Score 938; DB 2; L
Pred. No. 6.8e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 968; DB 2;
Pred. No. 1.7e-78;
9; Mismatches 64
                                                   Length 301;
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ŏ	63	63 RVSKEQGVLSLWRGNVANVIRYFFTQAFNFAFKDYFKNIF-PRYDQNTDFSKFFCVNILS 121
¥	120	120 GGAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNV 179
ŏ.	122	122 GATAGAISLLIVYPLDFARTRLASDIGK-GKDRQFTGLFDCLAKIYKQTGLLSLYSGFGV 180
¥	180	180 SVQGIIIYRAAYFGIYDTAKGML-PDPKNTHIVISMMIAQTVTAVAGLTSYPFDTVRRRM 238
ğ	181	181 SVTGIIVYRGSYFGLYDSAKALLFTNDKNTNIVLKWAVAQSVTILAGLISYPFDTVRRRM 240
¥	239	239 MMQSGRKG-TDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK 296
ř	241	241 MM/SGRKGKEBIQYKNTIDCWIKILRNEGFKGFFKGAWANVIRGAGGALVLVFYDELQK 299
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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P40941 arabidopsis
P12857 zea mays (m
P18239 saccharomyc
P25083 solanum tub
P31691 oryza sativ
P49382 kluyveromyc
P31167 arabidopsis
Q41629 triticum ae
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8 saccharomyc
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MITOCHONDRIAL INNER MEMBRANE. -!- SUBUNIT: Homodimer. -!- SUBCELLULAR LOCATION: Integral membrane protein. -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. -!- DOMAIN: COMPOSED to the mitochondrial carrier -!- SIMILARITY: Belongs to the mitochondrial carrier This SWISS-PROT entry is copyright. It is produced th	SEQUENCE OF 47-298 FROM N.A. TISSUB=Liver; TISSUB=124845; PubMed=2829183; HOULdsworth J., Attardi G.; "Two distinct genes for ADP/ATP translocase are expressed a level in adult human liver."; Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988)1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS	RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RA Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraja R., RA Mazzarella R.A., Schlessinger D., Chen E.Y.; RI Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases. RI [4] RP SEQUENCE FROM N.A. RA Becker M., Graves T., Ozersky P.; RI Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-87166056; PubMed=3031073; Battini R., Ferrari S., Kaczmarek L., Calabretta B., Cher Baserga R.; "Molecular cloning of a cDNA for a human ADP/ATP carrier growth-regulated."; J. Biol. Chem. 262:4355-4358(1987).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUB=Placenta; MEDLINE=90375457; PubMed=2168878; Ku DH., Kagan J., Chen ST., Chang CD., Baserga R., Wur "The human fibroblast adenine nucleotide translocator gene. cloning and sequence."; J. Biol. Chem. 265:16060-16063(1990).	13-AUG-1997 (Red. 05, Created) 01-OCT-1994 (Rel. 30, Last sequence update) 28-FBB-2003 (Rel. 41, Last annotation update) ADP,ATP carrier protein, fibroblast isoform (ADP/ATE (Adenine nucleotide translocator 2) (ANT 2). SLC25A5 OR ANT2. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; NCBI TaxID-9606;	H (C)	34 278 18.0 325 1 UCP5 MOUSE 35 276.5 17.9 322 1 GDC_RAT 36 276.5 17.9 702 1 CMCI_CABEL 37 276 17.8 678 1 CMCI_HVAN 38 274 17.7 325 1 UCP5 HUWAN 40 265.5 17.2 332 1 GDC_HUMAN 40 265 17.1 306 1 CK65 MOUSE 41 261.5 16.9 310 1 ODCI_YEAST 42 261 16.9 310 1 ODCI_YEAST 43 257.5 16.6 315 1 MFT_HUWAN 44 256 16.5 303 1 CK65_HUWAN 45 249.5 16.1 326 1 YEOS_SCHPO 46 265 16.5 303 1 CK65_HUWAN 47 261 16.9 310 1 ODCI_YEAST 48 257.5 16.6 315 1 MFT_HUWAN 49 256 16.5 303 1 CK65_HUWAN 40 265 16.5 303 1 CK65_HUWAN 41 256 16.5 303 1 CK65_HUWAN 42 261 16.9 310 1 ODCI_YEAST 43 257.5 16.6 315 1 MFT_HUWAN 44 256 16.5 303 1 CK65_HUWAN 45 249.5 16.1 326 1 YEOS_SCHPO 46 26 27 CKAPT 47 27 CWCL 48 27 CWCL 49 28 28 28 28 28 28 28 28 28 28 28 28 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
[1]
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Adenine nucleotide translocator SLC25A5 OR ANT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last annotation update) ADP,ATP carrier protein, fibroblast isoform (Adenine nucleotide translocator 2) (ANT 2).
                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
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    -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
    -!- SIMILARITY: Belongs to the mitochondrial carrier family.

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GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
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                                                                                                                                                                                                                           MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
                                                                                                                                            I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKRTQFWRYFAGNLASG
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llarity 98.3%;
Conservative
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Pred. No. 1e-1
3; Mismatches
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P51881; Q61311;
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D8 (Adenine nucleot:
GN APP, ATP CARTIEY:
D8 (Adenine nucleot:
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RE SEQUENCE FROM N.
RC TISSUE-Skeletal:
RA COSTET PONT N.
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RA Sheldon J.G.;
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RN [3]
RA STRAIN-129/59;
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Gene 254:57-66 (2000).
                                                                                                                                                                                                                                     use by non-profit institutions a modified and this statement is not entities requires a license agreem
                                                                           EMBL; U27316; AAC52838.1; -.
EMBL; U104004; AAA50090.1; -.
EMBL; X70847; CAAA50196.1; -.
EMBL; AF240003; AAF64471.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
ADP, ATP carrier protein, fibroblast is
(Adenine nucleotide translocator 2) (A
SLC25A5 OR ANT2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6; TISSUB=Brain; MEDLINE=97059403; PubMed=8903724;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ellison J.W., Li X., Francke U., Shapiro i Rapid evolution of human pseudoautosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                     Ween, the SWIBS AND THE TREE TREE TO THE BUTOPEAN BIOINFORMATICS Institutions as long by non-profit institutions as long by non-profit institutions as long by non-profit institutions as long by non-profit institutions as long by non-profit institutions as long by non-profit institutions as long by non-profit institutions as long by non-profit institutions as long by non-profit institute. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: CATALYZES THE EXCHANGE MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS
     MGI:1353496; S1c25a5
rPro; IPR002067; Mit or
rPro; IPR002030; Mit or
                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een, the Swiss Institute of Bioinformatics and the EMBE outstation surpean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                            s requires a license agreement (See an email to license@isb-sib.ch).
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(ANT 2).
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ADT3 BOVIN STANDARD, PRT; 298 AA.

p32007;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, isoform T2 (ADP/ATP t
nucleotide translocator 3) (ANT 3).

SLC25A6 OR ANT3.
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Best Local Similarity
                                                                          SEQUENCE FROM N.A.

MEDLINE-8929093; PubMed-2540808;

Powell S.J., Medd S.M., Runswick M.J., W.

"Two bovine genes for mitochondrial ADP/J

differences in various tissues.";

Biochemistry 28:866-873(1989).

-I- FUNCTION: CATALYZES THE EXCHANGE OF J

MITOCHONDRIAL INNER MEMBRANE.

-I- SUBCELLULAR LOCATION: Integral membra
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
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Multigene famil
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               inner membrane.
DOMAIN: COMPOSED OF
SIMILARITY: Belongs
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PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I PKBQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKRTQFWRYFAGNLASG
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ADP/ATP translocase
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There are no restrictions ng as its content is in

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collaboration

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MEDLINE=89236396; PubMed=2541251; Cozens A.L., Runswick M 7
                                                                                                                                                                                                  ADT3 HUMAN STANDARD; PKT; 270 Am.
P1235; O96C49;
01-OCT-1989 (Rel. 12, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADP,ATP carrier protein, liver isoform T2 (ADP/ATP ADP,ATP nucleotide translocator 3) (ANT 3).
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Eukaryota; Metazoa;
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PRINTS; PR00926; MITOCARRIER
PRINTS; PR00784; MIUNCOUPLING.
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
                                                                                                                               Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDBIKK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPPDTVRRRMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQGIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I PKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               equires a license agreement (S email to license@isb-sib.ch).
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                                                                                                                            Chordata;
Primates;
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                  Walker J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1458; D
Pred. No. 7.7e
L3; Mismatches
                                                                                                                            Craniata; Vertebrata;
Catarrhini; Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
.7e-121
                                                                                                                               Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage
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RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., High F.R.
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Richards A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Schein J.E., Jones S.J.M., Marra M.A.;
Thuman and mouse cDNA sequences.";
Thuman and mouse cDNA sequences.";
Thuman and mouse cDNA sequences.";
Thuman and mouse cDNA sequences.";
Thuman and sequences.";
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Margolin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Two distinct genes for ADP/ATP translocase are level in adult human liver.";
Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
-I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND MITOCHONDRIAL INNER MEMBRANB.
-I- SUBUNIT: Homodimer.
GO; GO:0005744; C:mitochondrial inner membrane translocase GO; GO:0005471; F:AFP/ADP antiporter activity; NAS. GO; GO:0006854; P:ATP/ADP exchange; TAS. InterPro; IPR002067; Mit_carrier. InterPro; IPR002030; Mit_uncoupling. InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC014775; AAH1
PIR; S03894; S03894.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J03592; AAA36750.1; EMBL; AY007135; AAG01998.
                                                                                                                                                                                                                                                                                                  MIM; 300151; -. MIM; 403000; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (Some send an email to license@isb-sib.ch).
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Strausberg R.L., Feingold E.A., Gi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SIMILARITY: Belongs to the mitochondrial carrier family:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88124845; PubMed=2829183; Houldsworth J., Attardi G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 36-298 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1, J0352; AAA36750.1; -...
AY057135; AAG01998.1; -...
BC007295; AAH07295.1; -...
BC007850; AAH07850.1; -...
BC008737; AAH08737.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: COMPOSED OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC008935; AAH08935.1;
BC014775; AAH14775.1;
                                                                                                                                                                                                                                                                                                                                                                                                             HGNC:10992;
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Biol. 206:261-280(1989)
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _MOUSE
_ADT1_MOUSE
P48962; Q621
01-FEB-1996
                                                                                                                                                                                                                   CONFLICT
                                              Laplace C.
Submitted
                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                             28-FBB-2003 (Rel. 41, Last sequence update)
15-SBP-2003 (Rel. 42, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (mANC1).
SLC25A4 OR ANT1 OR ANC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
  SEQUENCE FROM N.A.
                                                                      SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Muscle;
Laplace C., Costet P.;
                                                                                                                                                                                  homologs."
                                                                                                                                                                                                  Ellison J.W., Li X., Francke U., Shapiro L.J.; "Rapid evolution of human pseudoautosomal genes and their mouse
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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S; PR00926; MITOCARRIER
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; PS00215; MITOCH_CARRIER;
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Pred. No. 1.7e-120;
3; Mismatches 9;
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Sciurognathi; Muridae;
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F (IN REF. 3; AAH14
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Schaetel M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
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EMBL; X74510; CAA52616.1; -.
EMBL; AP240002; AAP64470.1; -.
EMBL; BC003791; AAH03791.1; -.
EMBL; BC0026925; AAH26925.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. These content is use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00153; mito carr; 3.
PRINTS; PR00926; MITOCOLARRIER.
PRINTS; PR00784; MITOCH_CARRIER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
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                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion; Inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
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MGD; MGI:1353495; S1c25a4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22388257; PubMed=12477932;
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translocase 1 and 2 genes.";
                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the mitochondrial carrier family.
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                         EMBL; X61667; CAAA3842.1; -.
EMBL; D12770; BAA02237.1; -.
PIR; IG0173; IG0173.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; Mitocarr; 3.
PRINTS; PR00926; MITOCARRIER.
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                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Isolation and characterization of cDNA clones and a genomic clone encoding rat mitochondrial adenine nucleotide translocator."; Biochim. Biophys. Acta 1152:192-196(1993).
-I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, MEDLINE=94002161; PubMed=8399300; Shinohara Y., Kamida M., Yamazaki N., Terada H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP_ATP carrier protein, heart/skeletal muscle isoform ;
translocase 1) (Adenine nucleotide translocator 1) (ANT
                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Nammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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EXTENT, IN BRAIN AND KIDNEY.
DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS
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01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart isoform T1 (ADP/ATP translocase (Adenine nucleotide translocator 1) (ANT 1).
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Aquila H., Misra D., Eulitz M., Kling
"Complete amino acid sequence of the
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                    MEDLINE=86295775; PubMed=3017341; Rasmussen U.B., Wohlrab H.;
                                                                                                                                  mitochondria.";
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  Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs
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Medd S.M., Runswick M.J.,
genes for mitochondrial ADF
in various tissues.";
Y 28:866-873(1989).
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                                                               207-297 FROM N.
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RESULT 9
ADT1_HUMA
ID ADT1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch carrier.
Pfam; PF00153; mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M24102; AAA30768.1; -. PIR; A43646; XWBO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unusually short 3'-noncoding sequence.";
ochem. Biophys. Res. Commun. 138:850-857(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Integral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                        SGRKGTDIMYTGTLDCWRKIARDEGGKAPFKGAWSNVLRGMGGAFVLVLYDEIKKY
                                                                                                                                                                                            QGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLITSYPFDTVRRRMMQ
                                                                                                                                                                                                                                      AAGATSLCFVYPLDFARTRLAADVGKGAAQREFTGLGNCITKIFKSDGLRGLYQGFNVSV
                                                                                                                                                                                                                                                                                                        PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASGG
                                                                                                                                                                                                                                                                                                                                      PKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGG
                                                                                                        SGRKGADIMYTGTVDCWRKIAKDEGPKAFFKGAWSNVLRGMGGAFVLVLYDEIKKF
                                                                                                                                                                       QGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQTVTAVAGLVSYPFDTVRRRMMQ
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89.9%;
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Science 289:7

"Role of adenine nucleotide translocator 1 in mtDNA Science 289:782-785(2000).

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robak S.A., McZewan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton B., Ketteman M., Wadan A., Rodrigues S., Sanchez A.,
RA Pahey J., Helton B., Ketteman M., Wadan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J., Scheutz J., Myers R.M.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Tenenan and mouse CDNA sequences "B., 1000 full-length
human and mouse CDNA sequences" and "B. 1000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1989 (Rel. 12, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last amotation update)
ADP,ATP carrier protein, heart/skeletal muscle isoform
translocase 1) (Adenine nucleotide translocator 1) (ANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of a leader peptide, divergence from a fibroblast translocator; and coevolution with mitochondrial DNA genes."; Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932;

"Transhard R.L.: Feingold E.A., Grouse L.H., Derge J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "cDNA sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE-89340499; PubMed=2547778;
Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
"A human muscle adenine nucleotide translocator gene has four
"A human muscle adenine nucleotide translocator gene has four
"A human muscle adenine al, and is differentially expressed.";
I blocated on chromosome 4, and is differentially expressed.";
                                                                                                                                                                     Houldsworth J., Attardi G.;
"Two distinct genes for ADP/ATP translocase are
level in adult human liver.";
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Mammalia; Eutheria;
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                                                      Comi G.P.,
                                                                        Kaukonen J.,
                                                                                           MEDLINE=20385067;
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                                                  Keranen J., Peltonen L.,
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K., Wade R.P., Shuster R., Wallace
a human skeletal muscle ADP/ATP tra
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Catarrhini; Hominidae;
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Suomalainen A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0006832; P:small molecule transport; TAS. InterPro; IPR002067; Mit_carrier. InterPro; IPR002030; Mit_uncoupling. InterPro; IPR001993; Mitoch_carrier.
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EMBL; J03593; AAA36751.1; -.
EMBL; J04982; AAA51736.1; -.
EMBL; BC008664; AAH08664.1;
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GO:0006091; P:energy pathways; TAS.
GO:0000002; P:mitochondrial genome maintenance; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO:0005887; C:integral to plasma membrane; GO:0005739; C:mitochondrion; TAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitochondrial DNA.
SIMILARITY: Belongs to the mitochondrial carrier family.
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I PKEQGFLS FWRGNLANV I RYFPTQALNFA FKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                 MGDHAWSFLKDFLAGGVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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l6; Mismatches
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RA Adams M.D., Celniker S.B., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barlew R.M., Basu A., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu B., Center A., Chandra I.,
RA Burtis K.C., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heimann T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Havrey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocase)
translocator) (ANT) (Stress sensitive B proteinsESS OR A/A-T OR CG16944.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang Y.Q., Davis A.W.,
Submitted (JAN-1997) to
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P91614; Q26254; Q95830; Q9VZ70;
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A Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
Al Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
Al Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
Al Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Al Merkulov G., Milshina N.V., Mobarry C., Morris J., McShrefi A.,
Al Mentulov G., Milshina N.V., Mobarry C., Morris J., McShrefi A.,
Al Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Al Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Al Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paccleb J.M.,
Al Melson D.R., Nelson K.A., Nixon K., Nixoski M.P., Sench H.,
Al Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Al Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
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Al Syirskas R., Tector C., Turmer R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Massarman D.A., Weinstock G.M., Weissenbach J.,
Al Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Al Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Al Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Al Meng X., Zhong F.M., Zhong M., Zhong G., Zhong L.,
Al Jeng X.H., Zhong F.M., Rubin G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y10618; CAA71628.1; -.
EMBL; AX003484; AAF47957.1; -.
EMBL; AX060978; AAL28526.1; -.
EMBL; AX070894; AAL48516.1; -.
FlyBase; FBgn0003360; sesB.
GO; GO:0005743; C:mitochondrial inner membrane; IE
GO; GO:0006899; F:mitochondrial transport; IMP.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR001993; Mitoch_carrier.
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MEDLINE-22426066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein P., Yu C., Cha
George R.A., Guarin H., Krommiller B., Pacleb J.M.,
Rubin G.M., Celniker S.B.;
"A Drosophila full-length cDNA resource.";
Cenome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
-!- FUNCTION: Catalyzes the exchange of ADP and ATP
mitochondrial inner membrane.
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SUBCELLULAR LOCATION: Integral membrane prote
inner membrane (By similarity).
DOMAIN: Composed of three homologous domains.
SIMILARITY: Belongs to the mitochondrial carr
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12 6 (POTENTIAL)
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7 G -> A (IN REF. 2)
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InterPro; IPR001993; Mitoch carrier.
Pfam; PF00153; mito_carr; a.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH CARRIER; 3.
Mitochondrion; Inner membrane; Repea
                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL of the European Bioinformatics Institute. There are no restrictive by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                                                                                                               Anopheles gambiae (African malaria mosquito)
Eukaryota; Metazoa; Arthropoda; Hexapoda; In
Neoptera; Endopterygota; Diptera; Nematocera
NCBI_TaxID=7165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last amotation updat
                                                                                                                                                                                                                                                                                                                                                                    "A cDNA encoding an ADP/ATP carrier from gambiae.";
                                                                                                                 EMBL; L11618; AAB04104.1;
EMBL; L11617; AAB04105.1;
                                                                                                                                                      entities requires a license agreement (Some send an email to license@isb-sib.ch).
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Beard C.B., Crews-Oyen A.E., Kuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translocator)
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SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                        inner membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p. 35, Last annotation update)
protein (ADP/ATP translocase)
31
93
136
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81.2%;
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                                                                                                                                                           is not removed. Usage by and to agreement (See http://www.isb-sib.
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Pred. No. 7.1e-103;
                                                                                                                                                                                                                                                                                                                                                                                                 Kumar V.K.,
          Repeat; Transmembrane; (POTENTIAL). (POTENTIAL).
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the mosquito
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era; Culicoidea; Anopheles
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T 01-JUL-1993 (Rel. 26, Created)
JT 01-JUL-1993 (Rel. 26, Last sequence update)
JT 01-JUL-1993 (Rel. 26, Last annotation update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DT ADP,ATP carrier protein (ADP/ATP translocase) (Adenine nucleo translocator) (ANT).
OS Chlorella kessleri.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellaceae; Chlorella.
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Best Local S
Matches 227
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hilgarth C., Sauer N., Tanner W.;

"Glucose increases the expression of the ATP/ADP translocator and glyceraldehyde-3-phosphate dehydrogenase genes in Chlorella.";

J. Biol. Chem. 266:24044-24047(1991).

-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.

-i- SUBUNIT: Homodimer (By similarity).
                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long are its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                              PIR; A41677; A41677.
InterPro; IPR002067; Mit carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; Mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                              EMBL; M76669; AAA33027.1;
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     MITOCH_CARRIER; 3.
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TRANSMEM 45
TRANSMEM 108
TRANSMEM 151
TRANSMEM 209
TRANSMEM 248
TRANSMEM 304
SEQUENCE 339
                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Texas Marker 1; TISSUE=Fiber;
Shin H., Brown R.M. Jr.;
Shin H., Brown R.M. Jr.;
"Two cDNA sequences for the adenine nucleotide translocator, CANT1
CANT2, from cotton fibers (Gossypium hirsutum).";
(In) Plant Gene Register PGR97-130.
(In) SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).
-i- SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GOSHI
ADT1_C
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidi
eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
28-FRB-2003 (Rel. 41, Last annotation update)
ADP,ATP carrier protein 1, mitochondrial precursor
translocase 1) (Adenine nucleotide translocator 1)
                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                               EMBL; AF006489; AAB72047.1;
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InterPro; IPR002067; Mit_carrier. InterPro; IPR001993; Mitoch_carri

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O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocase)
translocator) (ANT).
ANC1 OR SPBC530.10C.
                                                                                                                              Couzin N., Trezeguet V., Saux A.L., Lauquin G.J.M.;
"Cloning of the gene encoding the mitochondrial adenine nucleotide
carrier of Schizosaccharomyces pombe by functional complementation
Saccharomyces cerevisiae.";
Gene 171:113-117(1996).
                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae;
MEDLINE=21848401; PubMed=11859360; Wood V., Gwilliam R., Rajandream M.A., I Sgouros J., Peat N., Hayles J., Baker S.
                                                                                                                                                                                                                                      MEDLINE=96257204;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=972;
                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide; Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR00926; MITOCARRIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSLCFVYPLDFARTRLAAD--VGKAGAERBFRGLGDCLVKIYKSDGIKGLYQGFNVSVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVLSFWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPAIDFLMGGVSAAVSKTAAAPIERVKLLIQNQDEMIKSGRLSEPYKGIGDCFKRTIKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFAKDFLAGGVAAAISKTAVAPIERVKILLQVQ-HASKQITADKQVKGIIDCVVRIPKEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MMTSGKA---VKYKSSLDAFSQILKNEGGKSLFKGAGSNILRAIAGAGVLAGYDKLQLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MMQSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IIIYRAAYFGIYDTAK-----GMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSLLFVYSLDYARTRLANDAKAAKKGGERQFNGLVDVYRKTLKSDGIAGLYRGFNISCVG
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Pred. No. 2.3e
35; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 771;
No. 2.
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  Lyne M., Lyne
S., Basham D.,
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:3e-60;
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                        Stewart
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RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
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RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Gribert H.,
RA Woodward J., Volckaert G., Aert R., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Loga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Loga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe.",
RT Grymon S., Grymon S., Glow S., 
                                                                                                                                                                                        Matches
                                                                                                                                                                                                       Query Match
Best Local
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PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z49974; CAA90275.1; -
EMBL; AL023634; CAA19176.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitoch
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00153; mito
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GeneDB_SPombe; SPBC530.10c; -.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.-!- SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inner membrane.
DOMAIN: COMPOSED OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T40526; T40526
     124
                                           84
                                                                               64
                                                                                                                                                     7
                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                         ndrion;
                                                                                                                                                                                                                                                                                                                                                                                                        PR00926; MITOCARRIER.; 2.
                                                                                                                                       SFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADK---QYKGIIDCVVRIPK
   GATSLCFVYPLDFARTRLAADV--GKAGAERBFRGLGDCLVKIYKSDGIKGLYQGFNVSV
                                           EEGVISLWRGNTANVLRYFPTQALNFAFKDKFKKMF
                                                                TFFFDFMMGGVSAAVSKTAAAPIERVKLLIQNQ--DEMIRAGRLSHRYKGIGECFKRTAA
                                                                                                                                                                                                                                                          28
93
131
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222
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322
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                                                                                                                                                                                                       49.8%;
                                                                                                                                                                                                                                                                                                                                                                                       membrane;
                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                      51,
                                                                                                                                                                                     Pred. No. 2.3
                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                             (POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
8AC3D16A40F41AFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                    Repeat; Transmembrane; Transport. (POTENTIAL)
                                                                                                                                                                                                       770;
No. 2.
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                                                                                                                                                                                     DB 1; I
2.3e-60;
les 74;
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                                           -GYKKERDGYAKWFAGNLASGGAA
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                                                                                                                                                                                      Gaps
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GAASILFVYSLDYARTRLANDAKSAKKGGERQFNGLVDVYRKTYRSDGLRGLYRGFGPSV

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01-AUG-1992
01-AUG-1992
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SEQUENCE
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Sharpe J.A., Day A.;
"Structure, evolution and expression of the mitochondrial ADP/ATP translocator gene from Chlamydomonas reinhardtii.";
Mol. Gen. Genet. 237:134-144(1993).
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocase)
translocator) (ANT).
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PIR; S30259; S30259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as not removed. modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00153; mito_carr; 3. PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                    Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
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nterPro; IPR001993; Mitoch_carrier.
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                                                                                                                  Local
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       7
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                                                                                                                    Similarity
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                          SFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQ-HASKQITADKQYKGIIDCVVRIPKEQ
    PS00215; MITOCH_CARRIER; 2.
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Pred. No. 6e-60;
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(POTENTIAL).
2 (POTENTIAL).
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6 (POTENTIAL).
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                                                                                            Mismatches
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EVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGA 125

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                                                                                                                                 GIIIYRAAYFGIYDTAKG-MLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMMQ 241
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                         KY 297
                                                                              SGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEI-----K
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                                                     -GSAVKYNSSFHCFQEIVKNEGMKSLFKGAGANILRAVAGAGVLAGYDQLQVILLGK
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Search completed: December 18, 2003, 12:41:24 Job time: 9.34267 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, <u>1</u>8 derived by analysis of the total score distribution

SUMMARIES

9876	ารของส	Result No.
1463 1454 1454 1454	1543 1543 1543 1543 1543	Score
94.8 94.2 94.2 94.2	100.0 100.0 100.0	Query Match
298 298 298 298	298 298 298 298	Query Match Length DB
23 23 23	22222	B
AAO18516 AAY71032 AAU01199 AAU10379	AAY71033 AAM39641 AAU01200 AAU10380 AAM41427	ij
Human insulin rece Human adenine nucl Human adenine nucl Human adenine nucl	Human adenine nucl Human polypeptide Human adenine nucl Human adenine nucl Human-polypeptide	Description

03-NOV-1998; 08-SEP-1999;

98US-0185904. 99US-0393441.

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ALIGNMENTS

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RESULT 1
AAY71033
                                                                                  AAY71033;
Human adenine nucleotide translocator ANT3.
                                       29-AUG-2000 (first entry)
                                                                                                                          AAY71033 standard; Protein; 298 AA
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Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; notropic; antiParkinsonian; cytostatic; antidiabbetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzhetmer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber; parkinson's potic neuropathy; schizophoria; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome. 03-NOV-1999; 11-MAY-2000 Homo sapiens. WO200026370-A2 99WO-US25883. dystonia;

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AAM39641
ID AAM3
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Matches
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Ghosh SS;
Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                            Human polypeptide
                                                                                                                                   22-OCT-2001
                                                                                                                                                                                                         AAM39641 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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N-PSDB; AAD00521.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGATS1CFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                                                                                          QSGRKGADIMYTGTVDCWRKI FRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDBLKKVI
                                                                                                                                                                                                                                                                                                                                                                                                       VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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                                                                                                                                                                                                                                                                                                     QSGRKGAD IMYTGTVDCWRKI FRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                                                                                                                                                                                                                                                                                                                  VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 173-174; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       discloses a method to produce adenine nucleotide translocator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
llarity 100.0%;
Conservative 0
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                                                                                             SEQ ID
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                                                                                             2786.
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Pred. No. 4.6e-157;
; Mismatches 0;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, described as immune system suppression, assays for receptor activity, arthritis and inflammation, leukaemias and the structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                                      C.N.S disorders.
Note: The sequence
                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; SEQ ID NO 2786; 10078pp; English
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19-OCT-2000;
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DB; AAI58797.
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                                                                                                                                                                     1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQVKGIVDCIVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
Wang Z,
Zhou P,
               VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSMMIAQTVTAVAGVVSYPPDTVRRRMM
                                                                    GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                    I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
                                                                                                                     IPKEQGVLSFWRGNLANVIRYFFTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                        MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                  GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                 298
                                                                                                                                                                                                             100.0%; Score 1543; DB 22; ilarity 100.0%; Pred. No. 4.6e-157; Conservative 0; Mismatches 0;
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2000US-0598042.
2000US-0620312.
2000US-0653450.
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2000US-0693036.
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Wehrman T, 2
, Goodrich R,
                                                                                                                                                                                                                                                                                                        data
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, Xu C, Xue I
R, Drmanac R'
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241

QSGRKGADIMYTGTVDCWRKI FRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI

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                                                                                                                                                                         The present sequence represents human adenine nucleotide translocator-3 (ANT-3) protein. ANT proteins are mitochondrial permeability transloted (ANT-3) protein. ANT proteins are mitochondrial permeability transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (Ce.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter treatment of disease associated with altered mitochondrial function or treatment of diseases associated with altered mitochondrial function or diseases associated with altered mitochondrial encephalopathy, lactic acidosis, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke.
                                                   Query Match
Best Local Similarity
Matches 298; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; adenine nuclectide translocator-3; ANT-3; MTP; cyclophilin; mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-NOV-2000; 2000WO-US30535.
                                                                                                                                                                hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Velicelebi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MITO-) MITOKOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human adenine nucleotide translocator-3 (ANT-3) protein
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MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                                                               298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clevenger W,
3, Davis RE;
                                                       100.0%;
larity 100.0%;
Conservative 0
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                                                                                                                                                            disorders e.g. cancer,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wiley SE,
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                                                         0;
                                                     Score 1543; DB 22;
Pred. No. 4.6e-157;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andreyev AY,
                                                                                                                                                                and deafness.
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Frigeri
                                                                                          298;
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RESULT 4
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XX II-N
XX II-N
XX II-N
XX III-N
XX II
The invention relates to a recombinant expression construct (I) C comprising a regulated promoter operably linked to a nucleic acid c encoding an adenine nucleotide translocator (ANT) polypeptide. ANT CC proteins mediate the exchange of ATP synthesised in the mitochondrial CC matrix for ADP in the cytosol. (I) is useful for producing recombinant CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and CC culturing the host cell. (I) is also useful for targeting a polypeptide CC of interest to a mitochondrial membrane, where ANT polypeptide is CC expressed as a fusion protein with the polypeptide of interest. CC Recombinant ANT polypeptide, or cells expressing the polypeptide. ANT CC ligand is useful for determining the presence of an ANT polypeptide. CC useful for identifying an agent that binds to an ANT polypeptide. CC ANT from a biological sample, where the ANT ligand is covalently or non-cc covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson (
Ghosh SS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A CM, L. MOOS WH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Davis RE, Clevenger W, Wiley SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotide translocator 3 (ANT3).
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
19-JUG-2000;
14-SEP-2000;
                                                                                                                                               Tang
Wang
  Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                              Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; nerpoathy; central nervous system; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                               26-DEC-2000; 2000WO-US34263.
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                                                                                                                          Liu C,
Wang Z,
Zhou P,
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; 2000US-0662191.
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Wehrman T,
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Pred. No. 4.6
0; Mismatches
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Xue AJ,
nac RT;
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4.6e-157;
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Yang
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Pred. No. 5.2e-157;
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12-JAN-2001; 12-JAN-2001; 12-JAN-2001; 12-JAN-2001; 12-JAN-2001; 12-JAN-2001;

2001US-261226P. 2001US-261303P. 2001US-261304P. 2001US-261335P. 2001US-261336P.

11-JAN-2002; 2002WO-US01048.

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12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                  Sequence
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12-JAN-2001;
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DB; AAL48635.
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               QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
                                                                      VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPPDTVRRRMM
                                                                                                                                                                       I PKEQGVLS FWRGNLANVIRYFFTQALNFAFKDKYKQI FLGGVDKRTQFWRYFAGNLASG
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                                                      VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
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2001US-261531P.
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2001US-261461P.
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13; Mismatches 8;
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RESULT 7
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ID AAY7

AAY71032 standard; Protein;

298 AA.

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Indels

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Gaps

60 120

IPKEQGVLSFWRGNLANVIRYEPTQALNEAFKDKYKQIELGGVDKHTQFWRYFAGNLASG

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Best Loc
Matches
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                                                                                                              inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MIDD), and mycclonic epilepsy red ragged fibre syndrome. The present sequence is an adenine nucleotide translocator ANTZ from human brain.
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Ghosh SS;
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                                                                                                                                                                                                                                                                                                                                                                                         The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic against mitochondrial disease
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08-SEP-1999;
                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 45; Page 172-173; 175pp; English
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N-PSDB; AAD00520.
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/ Match 94.2%;
Local Similarity 92.6%;
les 274; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adenine nucleotide translocator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    di-phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotide translocator ANT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Davis
                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0185904.
99US-0393441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US25883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  de translocator; ANT2; mitochondria; ADP; ATP;
adenosine tri-phosphate; apoptosis; MPT; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clevenger W,
Score 1454; DB 21;
Pred. No. 1.7e-147;
3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wiley SE,
                                        DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miller
                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Szabo TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agents
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The present sequence represents human adenine nucleotide translocator-2 (ANT-2) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact vith other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (BTM) protein (e.g. ANT) fused to an energy transfer molecule (BTM) protein (c.g. The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of disease associated with altered mitochondrial function or treatment of disease associated with altered mitochondrial function or disease, functions, Parkinson's disease, Huntington's disease, Schizophrenia, cmitochondrial encephalopathy, lactic acidosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynuclectide encoding MPT polypeptide or cyclophilin polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-291054/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murphy AN, C
Velicelebi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitochondrial permeak mitochondrial core con Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; adenine nucleotide translocator-2; ANT-2; MTP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human adenine nucleotide translocator-2 (ANT-2) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                to energy transfer molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYFFDTVRRRMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGATSLCFVYPLDFARTRLAADVGKAGAERBFRGLGDCLVKIYKSDGIKGLYQGFNVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I PKEQEVLS FWRGNLANVI RYF PTQALNFAFKDKYKQI FLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clevenger W,
3, Davis RB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        permeability transition pore component; cell survival;
core component; mitochondrial related disorder; cancer;
isease; diabetes mellitus; hyperproliferative disorder.
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cell survival;
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Best Local
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                                                                                                                                                      Anderson C
Ghosh SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                           WPI; 2002-055598/07
N-PSDB; AAS16689.
                                                                                                                                                                                                                                                                                            Human; adenine nucleotide translocator; ANT; ss; mitochondrial matrix protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hyperproliferative disorders e.g. cancer,
                                                                                                                                                                                                    11-MAY-2000; 2000US-0569327
                                                                                                                                                                                                                      11-MAY-2001; 2001WO-US15416.
                                                                                                                                                                                                                                         15-NOV-2001.
                                                                                                                                                                                                                                                          WO200185944-A2
                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                        Human adenine nucleotide translocator 2 (ANT2).
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                                                                                                                                               Moos +
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                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                   OSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRWMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
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                                                                                                                                                                Davis
                                                                                                                                                                                                                                                                                                                                          (first
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                                                                                                                                                                                                                                                                                                                                                                              Protein;
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Pei
                                                                                                                                                                                                                                                                                                                                          entry
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                                                                                                                                                      Y, Carroll AK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1454; D
Pred. No. 1.7e
3; Mismatches
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                                                                                                                                                                Wiley SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and deafness
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                                                                                                                                                                 Miller
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                                                                                                                                                                 WS.
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                                                                                                                                                                 Szabo
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The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell culturing the host cell. (I) is also useful for targeting a polypeptide

for targeting a polypeptide

and

Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide

for producing adenine nucleotide regulated promoter linked to

Claim 44; Fig 2; 147pp;

English.

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RESULT 10
ABR41715
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28-MAR-2001;
29-MAR-2001;
29-MAR-2001;
16-MAY-2001;
17-MAY-2001;
17-MAY-2001;
19-JUN-2001;
20-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. Recombinant ANT polypeptide, or cells expressing the polypeptide, is useful for identifying an agent that binds to an ANT polypeptide, ANT ligand is useful for determining the presence of an ANT polypeptide, preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating ANT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT2.
                                                                                                                                                                                                                                                                                                cancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; infection; hormonal disorder; metabolic disorder; neurological disorder; asstrointestinal disorder; transport disorder; connective tissue disorder; drug screening; proteome analysis; gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
                                                                                                                                             27-MAR-2002;
                                                                                                                                                                                                           WO200297031-A2
                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                      organelle-associated
                                                                                                                                                                                                                                                                                   gene therapy; antisense therapy; genoticisease model; toxicological testing;
                                                                                                                                                                                                                                                                                                                                                                Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis; cancer; cell proliferative disorder; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABR41715;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSGRXGADIMYTGTVDCWRKI FRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKX 296
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 2001US-279619P.
2001US-2800667P.
2001US-280068P.
2001US-291280P.
2001US-291280P.
2001US-291829P.
2001US-291849P.
2001US-299428P.
2001US-299476P.
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                                                                                                                                                                                                                                                                                                                                                                                                              organelle-associated protein
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                                                                                                                                             2002WO-US10056
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                      protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1454; DB 23; Pred. No. 1.7e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₹
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Dufour GE, Hillman
Daughtery SC, Dam T
Peralta CH, David M
Flores V, Marwaha F
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                                                                                                                                                                                                                       (INCY-) INCYTE GENOMICS
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)B; ACC46652.
                                                                                                                                                                                           C, Dam TC,
David MH,
Marwaha R,
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                                                                                                                                                                                                                       INC.
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Liu TF, Nguyen DA,
Lewis SA, Chen AJ,
                                                                                                                                                                                            SA, Cho
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Urashka ME;
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Harris B;
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Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies

SEQ ID No 1250; 591pp; English.

CC sequences of the invention; recombinant vectors, host cells and commercial organisms comprising a dithp nucleic acid sequence; the CC recombinant production of DITHP proteins; antibodies specific for DITHP proteins; microarrays comprising dithp nucleic acid sequences; methods of greening dithp nucleotide and protein sequences; methods of screening CC for compounds which specifically bind a DITHP protein; and methods of assessing the toxicity of test compounds using a dithp hybridisation CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the CC diagnosis of a wide variety of conditions including cancer and other cell CC proliferative disorders; autoimmune or inflammatory disorders; bacterial, CC viral, fungal or parasitic infections; hormonal disorders; metabolic CC disorders; neurological disorders; gastrointestinal disorders; metabolic CC disorders; and connective tissue disorders. They may also be used to CC screen for modulators of protein activity or gene expression. DITHP proteins can additionally be used in analysis of the proteome of a tissue correction activity or gene expression. DITHP proteins can additionally be used in analysis of the proteome of a tissue correction activity or gene therapy of the disorders additioned above, as a source of antisense sequences, as a source of comencioned above, as a source of the protein activity and disease or knock in the generation of transgenic animal models of human disease or knock in the disorders in the disorders and contents in a total colories. The invention relates to novel human diagnostic and therapeutic polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded proteins (DITHP, ABR41136-ABR41812). The invention also to polynucleotide sequences at least 90% identical to the dithp Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO the generation of transgenic animal models of human disease or knock in humanised animals, in toxicological testing, and in transcript imaging. The present sequence represents a DITHP protein which is an organelleassociated protein. relates CDNA

Sequence 429 B

Similarity

24;

Length

429;

ftp.wipo.int/pub/published_pct_sequences.

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Matches 277
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                                                                 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                                                       MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                   I PKEQGVLS FWRGNLANVI RYF FTQALNFAFKD KYKQI FLGGVDKHTQFWRYFAGNLASG
                                                  GAAGATSI
                                                                                                     1PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQ1FLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                       Conservative
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95.2%;
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Pred. No. 2e-143;
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                                                  FRGLGDCLVKITKSDGIRGLYQGFSVS
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RESULT 11
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Best Local (
                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ant1; Adenine nucleotide translocator; cloning; screening; DNA Taq dideoxy terminator cycle sequencing; oxidative phosphorylation; probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy; hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy; lactic acidosis; degenerative muscle disease.
                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 39-40; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mice lacking heart-muscle adenine nucleotide translocator protein useful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-286608/25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     independent of ANT1.
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   61
                                                                13
                                                                                                                                                                                                                                                 264;
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                                                                                                                                                                                                                                                                                 Similarity
                                      I PKEQGVLS FWRGNLANVI RY F PTQALNFA FKDKY KQI FLGGVDKHTQFWRY FAGNLASG
   IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASG
                                                                                                                          MGDQALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                                             MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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                                                                                                                                                                                                                                                                                                                                                                           298
                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                              91.5%;
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                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                              Score 1412; DB 19;
Pred. No. 5.4e-143;
                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                 Indels
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61 65 μ. σ

QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASGGAAG QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG 124

120

AISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKE

ALSFLKDFLAGGIAAAVSKTAVAFIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKE

60

Query Match Best Local S Matches 263

al Similarity 263; Conserv

Conservative

91.1%;

Score 1406; DB 22; Pred. No. 2.3e-142; L7; Mismatches 12;

Indels Length

Gaps

293; <u>;</u>

Sequence

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RESULT 12
ABU53219
ID ABU53
XX ABU53
XX ABU53
XX ABU53
XX Human
XX Human
XX Human
XX Homo
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                                                                     This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids having the sequences of clones isolated from libraries different human tissues, useful in recombinant DNA methodologies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example III; Page 850; 1095pp; English
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28-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; gene therapy; vaccine; disease treatment; detection
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(ANT) proteins or ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial pore activity, for treating diseases diseases, cancer, psoriasis, diabetes, dystonia, leber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; adenine nucleotide translocator; ANT1; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MTT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia, diabetes; Leber's hereditary optic neuropathy; scrizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 44; Page 172; 175pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant construct encoding adenine nucleotide translocator , polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-NOV-1998;
08-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                   patent discloses a method to produce adenine nucleotide translocator
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DB; AAD00519.
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                       mitochondrial
mitochondrial
Alzheimer's di
                                                                                                                                                                                                                                                                                                                                                                                                Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin; mitochondrial permeability transition pore component; cell surviva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an adenine nucleotide translocator ANT1 from human brain.
                                                             New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises golynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule
                                                                                                                                                                   Murphy AN, Cl
Velicelebi G,
                                                                                                                                                                                                                                     03-NOV-1999;
                                                                                                                                                                                                                                                                 03-NOV-2000; 2000WO-US30535.
                                                                                                                                                                                                                                                                                                                    WO200132876-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human adenine nucleotide translocator-1 (ANT-1) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU01198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU01198 standard; Protein; 297
                                                                                                                                                                                                             (MITO-) MITOKOR.
                                                                                                                                                                                                                                                                                          10-MAY-2001.
                                                                                                                                2001-291054/30.
DB; AAS05901.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGATSLCFVYPLDFARTRLAADVGKSGTERBERGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGWGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSMNIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I PKEQGFLSFWRGNLANVIRY FPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM
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                                                                                                                                                                      Clevenger W,
G, Davis RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                   permeability transition pore component; cell core component; mitochondrial related disordisease; diabetes mellitus; hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥,
                                                                                                                                                                                                                                       99US-0434354.
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                                                                                                                                                                                  Wiley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1385.5; DB 2
Pred. No. 3.8e-140;
1; Mismatches 16;
                                                                                                                                                                                  SB,
                                                                                                                                                                                  Andreyev
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                                                                                                                                                                                                                                                                                                                                                                                                survival;
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Disclosure;

Fig

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186pp;

English

The present sequence represents human adenine nucleotide translocator-1 (ANT-1) protein. ANT proteins are mitochondrial permeability

interact

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AAU10378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, such as Alzheimer's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (BTM) protein (e.g. green fluorescent protein (GPP) or a FLASH sequence). The novel
                                Anderson CM, Davis RE, Clevenger W, W
Ghosh SS, Moos WH, Pei Y, Carroll AK;
                                                                                                                                                                                           11-MAY-2000; 2000US-0569327
                                                                                                                                                                                                                                                      11-MAY-2001; 2001WO-US15416
                                                                                                                                                                                                                                                                                                                                                                                      WO200185944-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; adenine nucleotide translocator; mitochondrial matrix protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human adenine nucleotide translocator 1 (ANT1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU10378 standard;
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                                                                                                                               (MITO-) MITOKOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyperproliterative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDT;VRRRMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.8%;
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Pred. No. 3.8
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                                                                 Wiley SE,
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                                                                 Miller SW,
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179

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DB 23;

Length

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CC comprising a regulated promoter operably linked to a nucleic acid comprising an adenine nucleotide translocator (ANT) polypeptide. ANT CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT CC matrix for ADP in the cytosol. (1) is useful for producing recombinant CC aNT polypeptide by transforming a prokaryotic or eukaryotic host cell and CC culturing the host cell. (1) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is CC expressed as a fusion protein with the polypeptide of interest. CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is CC useful for identifying an agent that binds to an ANT polypeptide, or CC ligand is useful for determining the presence of an ANT polypeptide, preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating CC ANT from a biological sample, where the ANT ligand is covalently or non-CC covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT1.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to nucleic acid encoding the polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-055598/07.
N-PSDB; AAS16688.
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297 AA;
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á 밁 Ś 멍 S 밁 S 밁 8 Query Match Best Local S Matches 260 241 240 180 181 121 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180 260; 61 61 μ 1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR Similarity GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYLDELKKVI 298 VQGIIIYRAAYFGVYDTAKGMLFDPKNTHIVVSWMIAQTVTAVAGVVSYFFDTVRRRMM 240 I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDBIKKYV 297 VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM Conservative 89.8%; 21; Score 1385.5; DB 2 Pred. No. 3.8e-140; 21; Mismatches 16; 16; Indels 1; Gaps 120 120 60 60 179

Search completed: Job time : 36.3729 December 18, 2003, 12:40:47

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Result
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/cgm2 6/ptodata/1/iaa/6B_COMB.pep:*
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           US-09-434-354-49
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US-08-470-868A-51
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ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 49
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
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APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Prigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert E.
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1543; DB 4; Best Local Similarity 100.0%; Pred. No. 4.5e-166; Matches 298; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING TITLE OF INVENTION: INTERACTIONS OF MITCCHONDRIAL COMPONENTS, AND FOR TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS FILE REFERENCE: 660088.433
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QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
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                                                                                                                                                                                                                                    Sequence 10, Application US/08961871
Patent NO. 6013858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: MacGregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6562563
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Holey, Sandra Eileen
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
FILE REFERENCE: 660088.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
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ORGANISM: Homo
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                              NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                            CITY: Boulder STATE: Colora
                                                                 ZIP: 80303
                                                                                        COUNTRY:
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5370 Manhattan Circle, Suite 201
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US-09-434-354-47
                  RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 91.5%;
Best Local Similarity 88.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
TELEPAX: (303) 499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (303) 499-808
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/
PILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                        QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                           VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
                                                                                                                                                       VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMM 240
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; Pred. No. 2.9e-151;
19; Mismatches 15;
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RESULT 4

IS-09-434-354-47

Sequence 47, Application US/09434354

Patent No. 656253

Patent No. 656253

Patent No. 656253

Patent No. 656253

PAPLICANT: Murphy, Anne N.

APPLICANT: Clevenger, William

APPLICANT: Andreyev, Alexander Y.

APPLICANT: Andreyev, Alexander Y.

APPLICANT: Pategeri, Luciano G.

APPLICANT: Davis, Robert E.

APPLICANT: Davis, Robert E.

TITLE OF INVENTION: INTERACTIONS AND METHODS FOR DETERMINING TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS FILE REFERENCE: 660088.433

CURRENT APPLICATION NUMBER: US/09/434,354

CURRENT PILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 54

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 47

LENGTH: 297

TYPE: PRT

ORGANISM: Homo sapien

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C13
CCURRENT APPLICATION NUMBER: US/09/996,243
CCURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR PILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/06250
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/066770
PRIOR PILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/066770
PRIOR PILING DATE: 1997-11-24
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Best Local S
Matches 260
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DR APPLICATION NUMBER: 60/065311
DR FILING DATE: 1997-11-13
DR APPLICATION NUMBER: 60/066770
DR FILING DATE: 1997-11-24
DR APPLICATION NUMBER: 60/075945
DR FILING DATE: 1998-02-25
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Baker, Kevin P.
Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
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Williams, P. Mickey
Wood, William I.
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Grimaldi, J. Christopher
Gurney, Austin_L.
                                                                                                                                                                                                                                                                                                             Tumas,
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Roy, Margaret Ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                               Napier, Mary A.
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                                                                                                                                                                                                                                                                                                          Daniel
                                                                                                                                                                                                                                                                                                                       Timothy A.
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87.2%; Pred. No. 2.96
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               APPLICATION NUMBER: 60/
PILING DATE: 1998-06-17
                                          APPLICATION NUMBER: FILING DATE: 1998-00
                                                                                     FILING DATE: 1998-00 APPLICATION NUMBER:
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FILING DATE: 1998-06-05
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                                                                         FILING DATE: 1998-06-16
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    60/089598
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APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17

APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17

APPLICATION NUMBER: 60/089600

FILING DATE: 1998-06-17

FILING DATE:

1998-06-17

FILING DATE:

1998-06-18

APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089801

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; ORGANISM: Mouse
US-09-188-930-339
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US-09-188-930-339
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SOFTWARE: FastSEQ for
SEQ ID NO 339
LENGTH: 469
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GENERAL INFORMATION:
                                                                                                                                                                                             Matches
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Best Local Similarity
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Best Local (
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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OP INVENTION: Compositions Isolated From Skin Cells
TITLE OP INVENTION: and Methods For Their Use
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CURRENT APPLICATION NUMBER: US/09/188,930A
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OR APPLICATION NUMBER: 60/091633
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091978
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/091982
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/092182
OR APPLICATION NUMBER: 60/092182
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130 FVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYRA 189
                                                     242
                                                                                                                         188 RHLVAGGGAGAVSRTCTAPLDRLKVLMOV-HASR-----SNNMCIVGGFTOMIREGGAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 SIYPMEVLKTRMA--LRKTG---QYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 LWRGNGINVLKIAPESAIKFMAYEQIKR--LVGSDQET---LRIHERLVAGSLAGAIAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188
                                                                                                                                                         10 KDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKEQGVLS
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                                                   LWRGNGINVLKIAPESAIKFMAYEOMKR--LVGSDQET---LRIHERLVAGSLAGAIAQS
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                                                                                                                                                                                           62; Mismatches 111;
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                                                                                                                                                                                                           Score 311; DB 3;
Pred. No. 1.7e-26;
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Pred. No. 7.8e-27;
0; Mismatches 115
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FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091478
FILING DATE: 1998-07-02

APPLICATION NUMBER: 60/091360

LING DATE: 1998-06-26

FILING DATE: 1998-06 APPLICATION NUMBER:

APPLICATION NUMBER: 60/090862

1998-06-26

60/090863

FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090696 APPLICATION NUMBER: 60/090695 APPLICATION NUMBER: 60/090694 FILING DATE: 1998-06-25

LING DATE: 1998-06-25

APPLICATION NUMBER: 60/091544

NUMBER: 60/091519

APPLICATION NUMBER: 60/090678 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090690 FILING DATE: 1998-06-25

FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090676 APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24

LING DATE: 1998-06-25

FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542

APPLICATION NUMBER: 60/090540 APPLICATION NUMBER: 60/090535 FILING DATE: 1998-06-24 FILING DATE: 1998-06-24 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472 APPLICATION NUMBER: 60/090445 PILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 APPLICATION NUMBER: 60/090435 PILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252

FILING DATE: 1998-06-22

APPLICATION NUMBER: 60/090246 APPLICATION NUMBER: 60/089952

FILING DATE: 1998-06-19

FILING DATE:

APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089908

1998-06-19

APPLICATION NUMBER: 60/089947

FILING DATE: FILING DATE:

APPLICATION NUMBER: 60/090355

1998-06-23 1998-06-22

APPLICATION NUMBER: 60/090431

1998-06-24

LING DATE:

1998-06-24

FILING DATE:

APPLICATION NUMBER: 60/090429

1998-06-23

1998-06-24

APPLICATION NUMBER: 60/090349 APPLICATION NUMBER: 60/090254

FILING DATE:

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US-09-312-283C-339
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                                                                                                                    GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
                                                                                                                                                                                           Sequence 118, Application US/09482273
Patent No. 6534631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 339
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ORGANISM: Mouse
-09-312-283C-339
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PILE REFERENCE: PZ030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT FILING DATE: 1999-05-14
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                                                                                                                                                                                                                                                                                                                                                                          238
                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 AYFGVYDTAKGMLPDPKNTHI------VVSWMIAQTVTAVAG-VVSYPFDTVRRR 237
                                                                                                                                                                                                                                                                                                                                   405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 FVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYRA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 RHLVAGGGAGAVSRTCTAPLDRLKVLMQV-HASR----SNNMCIVGGFTQMIREGGAKS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339, Application
o. 6573095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 FWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATSLC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 KDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKEQGVLS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88; Conservative
                                                                                                                                                                                                                                                                                                                                                                     MMMOSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFV-LVLYDELK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LWRGNGINVLKIAPESAIKFMAYEQMKR--LVGSDQET---LRIHERLVAGSLAGAIAQS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MQAQASIEGAPEVTMSSL--FKQİLRTEGAFGLYRĞLAPNFMKVIPAVSISYVVYENLK 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFV-LVLYDELK 295
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                                                                                                                                                                                                                                                                                                                            MQAQASIEGAPEVTMSSL--PKQILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLK 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIYPMEVLKTRMA--LRKTG---QYSGMLDCARRILAKEGVAAFYKGYIPNMLGIIPYAG 351
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Sleeman, Matthew
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Pred. No. 1.7e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 469;
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APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: No. 6403784el Human Uncoupling Proteins and TITLE OF INVENTION: Polymucleotides Encoding the Same FILE REFERENCE: LEX-0012-USA
CURRENT APPLICATION NUMBER: US/09/501,558
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 291
TYPE: PAT
ORGANISM: Homo sapiens
US-09-501-558-2
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US-09-501-558-2
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                                                                                                                        Query Match 18.4%; Score 283.5; DB Best Local Similarity 28.9%; Pred. No. 1.1e-23 Matches 87; Conservative 54; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander
APPLICANT: Mathur, Brian
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Best Local Similarity
Matches 87; Conserv
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SEQ ID NO 118
LENGTH: 335
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OTHER INFORMATION: Xaa
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EARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
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APPLICANT:
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                                                              KDFLAGGIAAAISKTAVAPIERVKLLLQVQHAS-----KQIAADKQYKGIVDCIVRIPKE
QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELKKV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIVVGVELPVYDITKKHLILSGMMGDTILTHFVSSF----TCGLAGALASNPVDVVRTRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VISSTIANPTDVLKIRMQA----QGSLFQGSMIGS-FIDIYQQEGTRGLWRGVVPTAQRA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGVLALYSGIAPALLRQASYGTIKIGIYQSLKRLFVERLEDET-----LLINMICGVVSG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPFVYGGLASIVABFGTFPVDLTKTRLQVQGQSIDARFKEI----KYRGMFHALFRICKE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KOFLAGGIAAAISKTAVAPIERVKLLLQVQHAS----KQIAADKQYKGIVDCIVRIPKE
                                        KPFVYGGLASITAECGTFPIDLTKTRLQIQGQTNDAKFKEI----RYRGMLHALVRIGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNORAIVGHVDLYKGTVDGILKMWKHEGFFALYKGFWPNWLRLGPWNIIFFITYEQLKRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zambrowicz, Brian
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Pred. No. 6.9e-24;
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                                                                                                                        Indels 31;
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RESULT 11
US-09-160-119-2
; Sequence 2, Application US/09160119A
; Patent No. 6316219
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US-09-160-119-4
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SEQ ID NO 4
LENGTH: 447
TYPE: PRT
ORGANISM: HOMO SAPIENS
S-09-160-119-4
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GENERAL INFORMATION:
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CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: EP 98401655.0 EARLIER FILING DATE: 1998-07-02 NUMBER OF SEQ ID NOS: 4
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APPLICANT: SOUCHET, MICHEL
APPLICANT: BRIL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: GH-30985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                               240 MQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEL 294
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                                                                                                                                                                                                                                                                                                                       156 YEGFFGLYRGLLPQLLGVAPEKAIKLTVNDFVRDKFMHKDGSVP-----LAAEILAG
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                                                                                                                                                                                                                                                                                                                                                      64 EQGVLSFWRGNLANVIRYFFTQALNFAFKDKYKQIFL---GGVDKHTQFWRYFAGNLASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.1%; ilarity 27.1%; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
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Sequence 2, Application US/09142565A
Patent No. 6187560
GENERAL INFORMATION:
APPLICANT: Lee James Beeley
APPLICANT: Kelly Paine
APPLICANT: Kelly Paine
APPLICANT: Robert James
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30002
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; ORGANISM: HOMO SAPIEN US-09-142-565-2
                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/142,565A.
CURRENT FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: 9704551.2
EARLIER FILING DATE: 1997-03-05
EARLIER APPLICATION NUMBER: 9705614.7
EARLIER FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: 97305305.1
EARLIER FILING DATE: 1997-07-16
EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 6
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                                    ; SEQ ID NO 2;
LENGTH: 312
TYPE: PRT
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FILE REFERENCE: GH-30985
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER FILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 4
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 674
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Best Local Similarity
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APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHET, MICHEL
APPLICANT: BRIL, ANTOINE
                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547 LQVAARAGQTTYSGVIDCFRKILREEGPKALWKGAGARVFRSSPQFGVTLLTYEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 MQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 YEGFFGLYRGLLPQLLGVAÞEKAIKLTVNDFVRDKFMHKDGSVP------LAABILAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFL---GGVDKHTQFWRYFAGNLASG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAV-AGVVSYPFDTVRRRMM
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ilarity 27.1%;
Conservative 4:
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Pred. No. 9.4e-23;
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180 488

546

434

Query Match Best Local Similarity

17.2%; 27.1%;

Score 265; DB 3; Pred. No. 1.5e-21;

Length 312

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US-08-518-878B-56
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                                                                                                           US-08-518-878B-56
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                                      Matchea
                                                                      Query Match
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                                                                                                                                                                                            TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                             TOPOLOGY: un
                                                                                                                                                                                                                                                                                                                  NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 10036-2711
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                                                       Local Similarity
                                                                                                                                                                           LENGTH:
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12 FLAGGIAAAISKTAVAPIERVKLLLQVQHASK---QIAADKQYKGIVDCIVRIPKEQGVL
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                                    74; ~ Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RMMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELK 295
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                                                                                                                                                                         299 amino acids
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VENTION: COMPOSITIONS AND METHODS FOR THE
VENTION: TREATMENT OF BODY WEIGHT DISORDERS,
                                                                                                                                                                                                                                               : (212) 790-9090
(212) 869-9741/8864
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                                                                                                                           unknown
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                                                                                                                                          single
                                                     16.2%; Score 250.5;
24.9%; Pred. No. 6e
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                                   Mismatches 146;
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                                    Indels
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                                 Gaps
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GENERAL INFORMATION:
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                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-UN-1995
                                                                                                                                                                                                                                                                                                                                       TELEX: 66441 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                            ATTURNET COTUZI, Laura A.

NAME: COTUZI, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositio
TITLE OF INVENTION: Treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                             LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 --NSALGQYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKRAL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 CFVYPLDFARTRLAADVGKSGTERBFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYR 188
  67
                                     69 SFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATSL 128
                                                                                                                  12 FLAGGIAAAISKTAVAPIERVKLLLQVQHASK---QIAADKQYKGIVDCIVRIPKEQGVL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 SLYNGLVÄGLQRQMSFASVRIGLYDSVKQFYTKG-SEHAS----IGSRLLÄGSTTGALAV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 SFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATSL 128
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SLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKG-SEHAS----IGSRLLAGSTTGALAV 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                   (212) 869-8864
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                            unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Compositions and Methods for the Treatment of Body Weight Disorders, Including Obesity
                                                                                                                                                                           16.2%;
                                                                                                                                                                                                                                                                                                                                                              56:
                                                                                                                                                            52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              7853-0031-999
                                                                                                                                                                           Score 250.5; DB
Pred. No. 6e-20;
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                                                                                                                                                                                               DB 2;
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US-08-518-878B-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 51
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                          Query Match
'Best Local Similarity
Matches 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 51, Application US/08518878B Patent No. 5702902
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,878B
FILING DATE: 23-AUG-1995
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: COTUZZÍ, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKST NUMBER: 78:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS,

NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) /30 TELEPHONE: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 --NSALGQYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYBQLKRAL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 GRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
  189 AAYFGVYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMOS 242
                                               132 AVAQPTDVVKVRFQAQ-ARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVN 190
                                                                         129 CFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 AAYPGVYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPPDTVRRRWMQS 242
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                                                                                                                                         77 SLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKG-SEHAS----IGSRLLAGSTTGALAV 131
                                                                                                                                                                                   69 SEWRGNLANVIRYEPTQALNEAFKDKYKQIFLGGVDKHTQEWRYFAGNLASGGAAGATSL 128
                                                                                                                                                                                                                                   17 FLGAGTAACIADLITFELDTAKVRLÓIÓGESQGPVRATVSAÓYRGVMGTILTMVRTEGPR 76
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                                                                                                                                                                                                                                                                        FLAGGIAAAISKTAVAPIBRVKLLLQVQHASK---QIAADKQYKGIVDCIVRIPKEQGVL
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                        16.2%; Score 250.5; DB 1; Length ilarity 24.9%; Pred. No. 6.3e-20; Conservative 52; Mismatches 146; Indels
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191 CÄELVTYDLIKDALLKANLMTDDLPCHFTSAFGAGFCTTVIÄS----PVDVVKTRYM--- 243

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244		243
244NSALGQYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKRAL 298		243 GRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELKKVI 298
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Search completed: December 18, 2003, 12:44:56 Job time : 13.3471 secs

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
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Perfect score:
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                                                                                                                                                                                                                                                                                      Published Applications AA:*

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1543
1 MTEQAISPAKDFLAGGIAAA......LRGMGGAFVLVLYDELKKVI 298
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1000 94.20 94.20 89.88 89.88 441.16 441.16 41.16	100.0	Query Match 1
298 298 298 298 299 299 1799 308 308 308	298	Query Match Length DB
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US-09-810-644-33 US-09-811-994-32 US-09-811-994-32 US-09-810-644-32 US-09-811-994-31 US-09-811-094-31 US-09-810-644-31 US-09-810-644-31 US-09-810-624-31 US-09-810-624-31 US-09-810-624-31 US-09-810-638-3561 US-10-032-585-7194 US-09-801-368-252 US-09-734-559-170 US-09-734-559-170 US-10-128-714-3338 US-10-128-714-8338	US-09-811-094-33	ID
Sequence 33, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 77, Appl Sequence 77, Appl Sequence 338, Ap Sequence 338, Ap Sequence 8338, Ap	Sequence 33, Appl	Description

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20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	21.1	21.6	23.8	23.8	27.4	Ψ	44.5	
469	469	469	469	469	469	469	469	469	469	469	469	469	469	469	469	469	469	469	469	469	469	384	410	477	475	87	132	677	
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US-09-997-653-289	US-09-989-734-289	-687	US-09-990-436-289	US-09-989-730-289	US-09-991-181-289	US-09-990-444-289	US-09-989-735-289	US-09-989-293A-289	US-09-992-598-289	US-09-989-721-289	US-09-990-456-289	US-09-993-604-289	US-09-991-163-289	US-09-990-442-289	US-09-991-073-289	US-09-989-732-289	US-09-989-731-289	US-09-989-727-289	US-09-989-279-289	US-09-989-723-289	US-09-989-722-289	US-10-094-749-1789	US-09-777-921A-5	US-09-777-921A-2	US-09-777-921A-4	US-09-864-761-36440	US-09-925-301-1459	US-10-259-165-192	
289,	289.	289,	289,	Sequence 289, App	289,	289,	289,	Sequence 289, App	289,	289,	289,	Sequence 289, App	289,	289,		289	e 289	289,	289,		289,	178	ភ	ν '	Sequence 4, Appli	36440	Sequence 1459, Ap	19:	

ALIGNMENTS

RESULT 1		
US-09-811-094-33	1-094-33	
; Sequence	ce 33, Application US/09811094	
; Patent 1	Patent No. US20010044144A1	
; GENERAL	GENERAL INFORMATION:	
; APPLICANT:	CANT: Anderson, Christen M.	
; APPLICANT	': Davis, Ro	
; APPLICANT	: Clevenger, Wi	
; APPLICANT		
; APPLICANT	: Willer, Scott	
; APPLICANT	: Szabo,	
; APPLICANT	••	
; APPLICANT	": Moos, I	
; APPLICANT	: Pei, 1	
; TITLE	OF INVENTION: PRODUCTION OF ADENING NUCLEOTIDE TRANSLOCATOR (ANT),	
; TITLE (OF INVENTION: NOVEL ANT LIGANDS AND SCREENING	
; FILE R	REFERENCE: 660088.420D4	
; CURRENT	NT APPLICATION NUMBER: US/09/811,094	
, CURREN		
NORTHER OF	CONTRACT OF THE MOST OF THE MARKET TO MAKE TO THE MOST OF THE MOST	
SEO ID NO 33	NO 33	
LENGT	LENGTH: 298	
; TYPE: PRT	: PRT	
; ORGAN	ORGANISM: Homo sapien	
US-09-811-094-33	1-094-33	
Query Match	100.0%;	
Matches	matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	٠.
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탕	1 MTEOAISFAKDFLAGGIAAAISKTAVAPIERVKLLLOVOHASKOIAADKOYKGIVDCIVR 60	
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Ş		
문	61 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKOKYKQIFLGGVDKHTQFWRYFAGNLASG 120	

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RESULT 2
US-09-810-644-33
; Sequence 33, Ap
; Patent No. US20
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                                                                                                                  RESULT 3
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Sequence 33, Application US/09185904A
Patent No. US20020177185A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 33
LENGTH: 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Anderson, C
APPLICANT: Davis, Ro.
APPLICANT: Clevenger,
APPLICANT: Wiley, Sar
APPLICANT: Willer, Sq
APPLICANT: Sabo, Ton
APPLICANT: Ghosh, Sou
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Homo sapien
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Local Similarity 100.0%;
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
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Pred. No. 1e-156;
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; ORGANISM: Homo US-09-811-094-32
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APPLICANT: Ghosh, Soumitra S.

TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE

TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING

TITLE OF INVENTION: THEREFOR

TILLE REFERENCE: 660088.420

CURRENT APPLICATION NUMBER: US/09/185,904A

CURRENT FILIG DATE: 1998-11-03

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 33

LENGTH: 298
                                APPLICANT: Pei, Yazhong
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REPERENCE: 660088.42004
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
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Matches 298; Conserv
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Best Local
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
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Wiley, Sandra Elleen
Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
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Pred. No. 1e-156;
; Mismatches 0
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Query Match Best Local Similarity

94.2%;

Score 1454; Pred. No. 3.

DB 9;).5e-147;

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US-09-810-644-32
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APPLICANT: Davis, Robert E
APPLICANT: Clevenger, Will
APPLICANT: Wiley, Sandra E
APPLICANT: Wiler, Scott W
APPLICANT: Szabo, Tomas R.
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SOFTWARE: FRASTSEQ for Windows Version
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
S-09-810-644-32
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CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
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Wiley, Sandra Bleen
Willer, Scott W.
Szabo, Tomas R.
Ghosh, Sounitra S.
Moos, Walter H.
Pei, Yazhong
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     QSGRKGTDIMYTGTLDCWRKIARDEGGKAPFKGAWSNVLRGMGGAFVLVLYDBIKK 296
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                                                                      VQGIIIYRAAYEGIYDTAKGMLFDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
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APPLICANT: Davis, Choert E.
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
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\US-09-185-904A-32
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                                                                                                                      APPLICANT: Anderson,
APPLICANT: Davis, Rol
APPLICANT: Clevenger
APPLICANT: Wiley, Sa
APPLICANT: Willer, Sc
APPLICANT: Szabo, Too
APPLICANT: Ghosh, Soo
APPLICANT: Moos, Wall
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; TYPE: PRT; ORGANISM: Homo sapien US-09-185-904A-32
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 660088.420
CURRENT EPILLAGION NUMBER: US/09/185,904A
CURRENT FILLING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
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Best Local Similarity
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APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
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QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
                                                                                                                                                                                          GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
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                                                                                IPKEQEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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US-09-810-644-31
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                                                                                                                                                                                                                                                                      FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
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Patent No. US20020012992A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
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TYPE: PR
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bei, Yazhong
| GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
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                                                                                                          MGDHAWSFLKDFLAGAVAAAVSKTAVAFIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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                                              I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
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Wiley, Sandra Eileen
Willer, Scott W.
Szabo, Tomas R.
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87.2%; Pred. No. 7.5e-140;
ative 21; Mismatches 16;
                                                                                                                                                                  89.8%; Score 1385.5; DB 9
87.2%; Pred. No. 7.5e-140;
ative 21; Mismatches 16;
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US-10-029-386-32501
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; ORGANISM: Homo
US-09-185-904A-31
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SEQ ID NO 31
LENGTH: 297
Sequence 32501, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEOMICA-X-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 31, Application US/09185904A Patent No. US20020177185A1 GENERAL INFORMATION:
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Best Local Similarity 87.2%;
Matches 260; Conservative 2
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APPLICANT:
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CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
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Willer, Scott W.
Szabo, Tomas R.
Szabo, Tomas R.
Ghosh, Soumitra S.
Ghosh, Soumitra S.
WYENTION: PRODUCTION OF ADENINE NUCLEOTIDE
NVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
                                                                                                                                                                                                                                                                                   QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                              VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
                                                                                                                                                                                                                                                                                                                                                                                                                GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPKEQGYLSFWRGNLANVIRYFPTQALMFAFKDKYKQIFLGGYDKHTQFWRYFAGNLASG
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                                                                                                                                                                                                                                                                                                                                     UGGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYFPDTVRRRWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMM
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                                                                                                                                                                                                                                                             QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clevenger, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Davis, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Christen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
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Pred. No. 7.5e-
21; Mismatches
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.5e-140;
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US-10-032-585-7194
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US-10-032-585-7194
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APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVERTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7194
LENGTH: 301
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 32501
LENGTH: 179
                                                                                                                                                                                                                                                                                                                 Matches
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Best Local (
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CURRENT FILING DATE: 2001-12-20
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN BAULT LIVER, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96

OTHER INFORMATION: SWISSPROT HIT: P05141, EVALUE 2.00e-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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Local Similarity 93.3%;
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                                                                             126 TSLCFVYPLDFARTRLAADV--GKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152;
  184
                                            123
                                                                                                                                     65
                                                                                                                                                                                                                                                                                                             tch 51.1%; Score 788.5; DB 12; Length 301; al Similarity 54.7%; Pred. No. 6.3e-76; 162; Conservative 42; Mismatches 83; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 VQHASKQIAADKQYKGIVDCIVRIPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQ 97
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IIIYRAAYFGVYDTAKG-MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMQS 242
                                                                                                                                     GVVSFWRGNTANVIRYFPTQALNFAFKOKFKAMF--GFKKDENYWKWFAGNLASGGLAGA 122
                                                                                                                                                            GVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                                                    NPFVDPMMGGVSAAVSKTAAAPIERVKLLIQNQDEMIKQGKLEKRYTGIVDCFKKTAADE 64
                                                                                                                                                                                                                                              SFAKDFLAGGIAAAISKTAVAPIBRVKLLLQVQ-HASKQIAADKQVKGIVDCIVRIPKBQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDCLVKITKSDGIRGLYQGFSVSVQGIIIYRAAYFGVYDTAKG 200
                                          TSLAFVYSLDYARTRLANDAKSSKGDGKREFNGLVDVYKKTLASDGIAGLYRGFGPSVIG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFLGGVDKHTQFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IFLGGVDKRTQFWLYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGL
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Pred. No. 1.2e-78;
6; Mismatches 5;
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RESULT 13
US-09-734-569-170
US-09-734-569-170; Sequence 170, Application US/09734569; Patent No. US20020064816A1; GENERAL INFORMATION:
; APPLICANT: Lerchl, Jens
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 252
LENGTH: 318
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Best Local :
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APPLICANT: Silva, Jeff
APPLICANT: Sulmers, Bric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR PILING DATE: 2000-01-19
PRIOR PILING DATE: 2000-01-19
PRIOR PILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
NUMBER OF SECOLIN NOC. 440
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                    126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159;
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                                                                                                                                                                                                                                                                                                                                                                                                                            66 GVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGA 125
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                                                                                                                                                                                           GRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
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                                                                                                                                                                      GQA---VKYDGAFDCLRKIVAAEGVGSLFKGCGANILRGVAGAGVISMYDQLQMIL
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Milne, Todd
No. US20020128250Alman,
Royer, John
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Madden, Kevin
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t, Peter
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Pred. No. 6.8e-73;
"" matches 86;
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RESULT 14
US-10-128-714-3338
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           CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
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SEQ ID NO 170
LENGTH: 386
TYPE: PRT
ORGANISM: Physcomitrella patens
                                                                                                                                                                       APPLICANT: Jiang, Bo
APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Exoshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
FILE REFERENCE: 10182-018-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved TITLE OF INVENTION: in the synthesis of carbohydrates FILE REFERENCE: BASF-NAS-1332-99-US CURRENT APPLICATION NUMBER: US/09/734,569 CURRENT FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 60/171,101 PRIOR APPLICATION NUMBER: US 60/171,101
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APPLICATION NUMBER: US 60/303,899
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157; Conserv
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Reski, Ralf
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Bischoff, Friedrich
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Petra
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53.4%; Pred. No. 1.36
tive 44; Mismatches
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PRIOR FILING DATE: 2001-07-09
PRIOR PPLICATION NUMBER: US 60/
PRIOR PILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: Patentin version 3.1
SEQ ID NO 3338
LENGTH: 308
TYPE: PRT
                                                                                         ; ORGANISM: Aspergillus fumigatus US-10-128-714-8338
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US-10-128-714-8338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Ecoshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                  SEQ ID NO 8338
                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8338, Application US/10128714 Publication No. US20030119013A1
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NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 50/305/05/
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
                                                                                                                                     LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 10182-018-999
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47.8%; Score 737; DB 15;
51.7%; Pred. No. 2.1e-70;
ative 47; Mismatches 85;
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Matches 154;

Indels

12;

Gaps

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Qy 7 SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPK 63	Search Job tim	문	Ş	D.	Ş	Db	φ	망	ş	皮	Ş	
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Listing first 45 summaries
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  Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
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S31931
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344.5	363	368	369.5	370.5	372	381	383	520.5	681.5	734.5	737.5	739.5	742	742.5	743
22.3	23.5	23.8	23.9	24.0	24.1	24.7	24.8	33.7	44.2	47.6	47.8	47.9	48.1	48.1	48.2
332	348	475	381	415	358	352	325	327	298	379	309	386	382	385	379
N	N	N	N	N	N	N	N	N	N	N	N	N	N	μ	N
T47703	D84798	T50686	T51158	T48171	T45934	T01729	T04273	T51577	T24029	S21313	A24849	S14874	S33630 .	S29852	T04608
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Ca-dependent solu	probable mitochon	peroxisomal	hypothetic	hypothetical	hypothetica	mitochondrial	hypothetical prote	ADP/ATP translocas	hypothetical prote	ADP, ATP carrier	ADP, ATP carrier	ADP, ATP carrier	ADP, ATP carrier	ADP, ATP carries	ADP, ATP carrier

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology P carrier pr C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein P carrier pr P;2-298/Product: ADP,ATP carrier protein #status predicted MATP: AMP; ATP carrier protein #status predicted MATP: AMP; ATP carrier protein repeat homology MACP1 etical prote P;110-202/Domain: ADP,ATP carrier protein repeat homology MACP2 etical prote P;207-298/Domain: ADP,ATP carrier protein repeat homology MACP2 etical prote P;207-298/Domain: ADP,ATP carrier protein repeat homology MACP2 etical prote P;207-298/Domain: ADP,ATP carrier protein repeat homology MACP2 etical prote P;207-298/Domain: ADP,ATP carrier protein repeat homology MACP2 etical prote P;207-298/Domain: ADP,ATP carrier protein repeat homology MACP2 etical prote P;207-298/Domain: ADP,ATP carrier protein repeat homology MACP2 etical prote P;207-298/Domain: ADP,ATP carrier protein repeat homology MACP2 etical prote P;207-298/Domain: ADP,ATP carrier protein repeat homology MACP2 etical prote P;207-298/Domain: ADP,ATP carrier protein repeat homology MACP2 etical prote P;207-298/Domain: ADP,ATP carrier protein repeat homology MACP2 etical prote P;207-298/Domain: ADP,ATP carrier protein repeat homology MACP2 etical prote P;207-298/Domain: ADP,ATP carrier protein repeat homology MACP2 etical prote P;207-298/Domain: ADP,ATP carrier protein repeat homology MACP2 etical protein repeat homology MACP2 etical protein repeat homology MACP3 etical protein repeat homology MACP3 etica	carrier pr nucleotide carrier pr carrier pr	RESULT 1 S03894 ADP, ATP carrier protein T3 - human N,Alternate names; ADP, ATP carrier protein T2 (misidentification); mitochondrial ADP, ATP C;Species; Homo sapiens (man) C;Accession; S03894; B28116 R;Cozens, A.L.; Runswick, M.J.; Walker, J.E. J. Mol. Biol. 206, 261-280, 1989 A;Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr A;Accession: 803894 A;Reference number: 803893; MUID:89236396; PMID:2541251 A;Accession: 803894 A;Residues: 1-298 <coz> R;Houldsworth, J; Attardi, G. Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988 A;Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a A;Resience: 1298: man. 894197; MUID:88124845; PMID:8829183 A;Accession: B28116 A;Accession: B2816 A;Accession: B2816 A;Accession: B2816</coz>	Seconds 35 734.5 47.6 379 2 S23313 ANP,ATP car. 36 681.5 44.2 298 2 T24029 hypothetica. 37 520.5 33.7 327 2 T51577 ADP/ATP tran 38 383 24.8 325 2 T04273 hypothetica. 39 381 24.7 352 2 T04273 hypothetica. 40 372 24.1 358 2 T45934 hypothetica. 41 370.5 24.0 415 2 T45151 hypothetica. 42 369.5 23.9 381 2 T51158 hypothetica. 43 368 23.8 475 2 T50686 peroxisomal 44 363 23.5 348 2 D84798 probable mi 45 344.5 22.3 332 2 T47703 Ca-dependen
GDE	expressed at the mRNA level in a	ification); mitochondrial ADP,A t_change 17-Mar-2000 or human mitochondrial ADP/ATP (ADP, ATP carrier pr hypothetical prote ADP/ATP translocas hypothetical prote mitochondrial solu hypothetical prote hypothetical prote hypothetical prote peroxisomal Ca-dep probable mitochond Ca-dependent solut

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N;Alternate names: mitochondrial ADP,ATP translocase 2
(;Species: Homo sapiens (man)
(;Species: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
(;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
(;Accession: A29132; C28116
R;Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga
J. Biol. Chem. 262, 4355-4359, 1987
A;Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is graph approximate the sequence number: A29132; MUID:87166056; PMID:3031073
A;Accession: A29132; MUID:87166056; PMID:3031073
                                                          A;Molecule type: mRNA
A;Residues: 1-298 <BAT>
A;Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
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A;Title: Two bovine genes for mitochondrial ADP/ATP translocase A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Accession: B43646
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A;Title:
                    R;Houldsworth, J.; Attardi, G. Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
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R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker,
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Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
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Two distinct genes for ADP/ATP translocase
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Pred. No. 3.3e-126;
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A;Map position: Xq13-Xq26
A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein C;Keywords: ADP,ATP carrier protein repeat homology <ACP1>
F;10-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A;Accession: C28116
A;Molecule type: mRNA
A;Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
A;Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1;
                                                                                 A;Introns: 37/3; 200/1; 247/1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; transmembrane protein C;Keywords: duplication; transmembrane protein F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACPl>F;110-202/Jomain: ADP,ATP carrier protein repeat homology <ACP2>F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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C;Species: Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA43842.1; PID:g400427
                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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                                                                                                                                                                                                                   Gene: ant
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                    92.3%;
  18;
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Score 1424; DB 2;
Pred. No. 2e-118;
8; Mismatches 13;
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Pred. No. 4.5e-121;
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A;Residues: 208-298 cARA>
A;Residues: 208-298 cARA>
A;Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1;
R;Aquila, H; Misra, D.; Eulitz, M.; Klingenberg, M.
R;Aquila, H; Misra, D.; Eulitz, M.; Klingenberg, M.
Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
A;Title: Complete amino acid sequence of the ADP/ATP carrier
A;Reference number: A03181; MUID:82188267; PMID:7076130
A;Accession: A03181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP, ATP carrier protein T1 - bovine
N;Alternate names: ADP/ATP translocase T1
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1993 #sequence revision 22-Jul-1994 #text_change
C;Accession: A43646; A24822; A03181; A61343; S69369
C;Accession: A43646, S.M.; Runswick, M.J.; Walker, J.E.
Blochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase
A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Accession: A43646
A;Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP A;Note: located in the inner mitochondrial membrane C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; m F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1> F;110-202/Jomain: ADP,ATP carrier protein repeat homology <ACP2> F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                  Bur. J. Blochem. 227, 730-733, 1995
A;Title: [(3)H]7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial A;Reference number: S69369; MUID:95172058; PMID:7867632
A;Accession: S69369
A;Molecule type: protein
A;Residues: 49-63;154-168 <OET>
C;Comment: This protein is synthesized in the cytosol and transported into the mitoch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 205-298 <BAB>
R;Oettmeier, W.; Masson, K.; Kalinna,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: residue 52 may be methyllysine R; Babel, W.; Wachter, E.; Aquila, H.; Klingenberg, M. Biochim. Biophys. Acta 670, 176-180, 1981
A; Title: Amino acid sequence determination of the ADP, ATP A; Reference number: A61343; MUID:82046808; PMID:6271240
A; Accession: A61343
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                                                                                                                                                                                                                      C;Complex: homodimer
C;Function:
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A;Residues: 2-51,'X',53-70,'X',72-109,'X',111-298
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A;Accession: A24822
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A;Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M24102; NID:g529414; R;Rasmussen, U.B.; Wohlrab, H.
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A;Gene: ANC1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein:
C;Keywords: duplication; transmembrane protein
C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP,ATP carrier protein T1 - mouse
N;Alternate names: adenine nucleotide c
;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision
C;Accession: S37210
R;Laplace, C.; Costet, P.
submitted to the EMBL Data Library, Seg
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C;Genetics:
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A; Residues: 1-298 < LAP>
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QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                       I PKEQGVLSFWRGNLANVI RYFPTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
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llarity 89.3%;
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Pred. No. 3.1e-
L9; Mismatches
                                                                                                                                                                                                                                                                                                                                                     Score 1418; DB 2;
Pred. No. 6.9e-118;
9; Mismatches 14;
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241

QSGRKGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 298

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ADP,ATP carrier protein T1 - human
ADP,ATP carrier protein T1 - human
N,Alternate names: mitochondrial ADP,ATP translocase 1
C;Species: Homo sapiens (man)
C;Spate: 17-Mar-2000 #sequence revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: A44778; S03893; \bar{A}39891; A28116
R;Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.
R;Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.
J. Biol. Chem. 264, 13998-14004, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 4035-4035
A;Map position: 4045-4035
C;Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology C;Superfamily: ADP, ATP carrier protein; mitochondrion; transmembrane protein C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;2-299/Froduct: ADP, ATP carrier protein #status predicted <AMT> F;5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1> F;110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2> F;110-209/Domain: ADP, ATP carrier protein repeat homology <ACP3>
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R,Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A,Title: cDNA sequence of a human skeletal muscle ADP/ATP t. A,Reference number: A39891; MUID:88041149; PMID:2823266
A,Recession: A39891
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J. Mol. Biol. 206, 261-280, 1980; Walker and the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second sec
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A;Title: A human muscle adenine nucleotide translocator gene has four exons,
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A;Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level A;Reference number: A94197; MUID:88124845; PMID:2829183
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A;Residues: I-15,'A','I-146,'RR',149,151-226,'L',228-298 <NEC>
A;Cross-references: GB:J02966; NID:g339919; PIDN:AAA61223.1; PID:g339920
A;Experimental source: clone pHMANT
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A;Residues: 1-37 <HOU>
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PLDFARTRLAADVGKGAAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
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A/Cross-references: EMBL:Z21814; EMBL:Z21815 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein C;Keywords: duplication; transmembrane protein F;7-101/Domain: ADP,ATP carrier protein repeat homology <ACP1>

repeat homology

ADP, ATP carrier protein - African malaria mosquito (;Species: Anopheles gambiae (African malaria mosquito) C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #tex C;Accession: S31935; S31936 R;Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H. submitted to the EMBL Data Library, February 1993 A;Description: A cDNA encoding an ADP/ATP carrier from

from the

mosquito Anopheles gambiae

#text_change 10-Sep-1999

S31935 RESULT

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A; Reference number: S31935 A; Accession: S31935

A; Molecule type: DNA A; Residues: 1-301 <BEA> A;Status: preliminary

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RESULT 8
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein of;Keywords: duplication; transmembrane protein
C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP>F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP>F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A; Accession: S31814
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                                                                                                                                             GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFKGLGDCLVKIYKSDGIKGLYQGFNVS
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                                                                       VQGIIIYRAAYFGIYDTAKGMLPDPXNTHIFISHMIAQSVTLVAGLTSYPFDTVRRRMMM
                                                                                                           VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
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89.2%;
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Pred. No. 9.8e-117;
6; Mismatches 16;
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A; Map position: 4
A; Introns: 4/1; 191/2
C; Superfamily: ADP, ATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein K01H12.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
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A;Experimental source: clone K01H12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-313 <WIL>
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Best Local Similarity
Matches 207; Conser
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Best Local
                                                                                                            188
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263
                             247 ADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
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                                                                                          RAAYFGVYDTAKGML-PDPKNTHIVVSMMIAQTVTAVAGVVSYPFDTVRRMMMQSGRKG
                                                                                                                                                                     LCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIY
                                                                                                                                                                                                                                                  LSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTEQA--ISFAKDFLAGGIAAAISKTAVAFIERVKLLLQVQHASKQIAADKQYKGIVDCI 58
                                                                                                                                             LCFVYPLDFARTRLAADVGKA-NEREFKGLADCLVKIAKSDGPIGLYRGFFVSVQGIIIY
                                                                                                                                                                                                                        AALWRGNLANVIRYFPTQALNFAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSVQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRM 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRIPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLA 118
                                                                                                                                                                                                                                                                                                   FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASLTIAADKRYKGIVDVLVRVPKEQGY
                                                                                                                                                                                                                                                                                                                       FAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKEQGV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGGAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTKKADPYGFAKDFLAGGISAAVSKTAVAPIERVKLLLQVQAASKQIAVDKQYKGIVDCF
                                                                      RAAYFGMFDTAKMVFTADGKKINFFAAWAIAQVVTVGSGIISYPWDTVRRRMMMOSGRK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMQSWPCKSEVMYKNTLDCWVKIGKQEGSGAFFKGAFSNVLRGTGGALVLVFYDEVKALL:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRIPKEQGIGAFCGGNLANVIRYFPTQALNFAFKDVYKQVFLGGVDKNTQFWRYFLGNLG 120
-DVLYKNTLDCAVKIIKNEGMSAMFKGALSNVFRGTGGALVLAIYDBIQKFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSVQGIIIYRAAYFGCFDTAKGMLPDPKNTSIFVSWAIAQVVTTASGIISYPFDTVRRRM
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                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     carrier protein; ADP,ATP carrier protein repeat
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77.0%;
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70.9%;
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; Pred. No. 1.7e-84;
29; Mismatches 52;
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Pred. No. 3.6e-97;
23; Mismatches 44;
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 313;
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A; Map position: 3
A; Introns: 20/1; 41/3;
C; Superfamily: ADP, ATP
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                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T27E9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat
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                                                                                                                                                                            A;Cross-references: EMBL:Z82059; PIDN:CAB04874.1; GSPDB:GN00021; A;Experimental source: clone T27E9
                                                                                                                                                                                                                                                                              A; Reference number: Z20024
A; Accession: T25371
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A; Residues: 1-313 <GEI>
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submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid T01B11.
A;Reference number: Z20099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: T25850
R; Geisel, C., Stell
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                                                                                                                                       A;Gene: CESP:T27E9.1
                                                                                                                                                                                                                      A;Residues: 1-300 <WIL>
                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                       A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, November
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                                       Query Match
                                                                                                                                                          Genetics:
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  Matches 202;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALWRGNLANVIRYPPTQALNPAFKDYKNIPQKGLDKKKDPWKFFAGNLASGGAAGATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAAYFGMFDTAKMVFTADGKKLNFFAAWAIAQVVTVGSGILSYPWDTVRRRMMQSGRK-
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  Conservative
                                                                             115/2 carrier protein; ADP,ATP carrier protein
                  67.3%; Score 1038; DB 2; 69.2%; Pred. No. 3e-84;
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    Mismatches
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                                                                                                                                                                                                                                                           GB/EMBL/DDBJ
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    49;
                                       Length 300;
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  Indels
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A;Map position: 1
C;Superfamily: ADP,A7
F;9-103/Domain: ADP,F
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A;Experimental source: strain Bristol N2; clone W02D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-300 <LET>
A;Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: Z18308
A; Accession: T15206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, May 1997 A;Description: The sequence of C. elegans co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
;Accession: T15206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology 9-103/Domain: ADP,ATP carrier protein repeat homology <ACR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession:
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                                                                                                       MMMQSGRK--DILYKNTLDCVRKIVKNEGITALYKGGLSNVFRATGGALVLTIYDEIQHL
                                                                                                                                      MMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKV
                                                                                                                                                                            VSVQGIIIYRAAYFGMFDTAKTLYSTDGQKLNFFTTWAIAQVGTVGSGYLSYPWDTVRRR
                                                                                                                                                                                                VSVQGIIIYRAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPPDTVRRR
                                                                                                                                                                                                                                                SGGAAGATSLCFVYPLDFVRTRLGADVGK-GVDREFQGLTDCFVKIVKSDGPIGLYRGFF
                                                                                                                                                                                                                                                                  SGGAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFS
                                                                                                                                                                                                                                                                                                                     ARVPKEQGYAAFWRGNLANVLRYFPTQALNFAFKDTYKKMFQEGIDKNKEFWKFFAGNLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.4%; Score 993.5; DB 2 64.8%; Pred. No. 2.6e-80;
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RESULT 14

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RESULT 15
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A,Molecule type: mRNA
A;Residues: 1-339 <HIL>
A;Residues: 1-339 <HIL>
A;Cross-references: GB.M76669; NID:g516596; PIDN:AAA33027.1; PID:g516597
A;Cross-references: GB.M76669; NID:g516596, ATP carrier protein; ADP,ATP carrier protein; ADP,ATP carrier protein for cykeywords: duplication; homodimer; mitochondrion; transmembrane protein f;38-134;Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;144-235/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;241-329/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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ADP,ATP carrier protein - Chlorella kessleri
C;Species: Chlorella kessleri
C;Species: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C;Accession: A41677
C;Accession: A41677
                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-301 <HAT's
A;Residues: 1-301 <HAT's
A;Residues: 1-301 <HAT's
A;Residues: 1-301 <HAT's
A;Residues: 1-301 <HAT's
C;Coss-references: EMBL:X83551; NID:g623334; PIDN:CAA58541.1; PID:g623335
A;Cross-references: EMBL:X83551; NID:g623334; PIDN:CAA58541.1; PID:g623335
C;Superfamily: ADP,ATP carrier protein; ATP carrier protein repeat homology <ACP1>
F;61-102/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;112-203/Domain: ADP,ATP carrier protein repeat homology <ACP2>
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP,ATP carrier protein - malaria parasite (Plasmod N;Alternate names: ADP/ATP transporter C;Species: Plasmodium falciparum C;Date: .07-May-1995 #sequence_revision 01-Sep-1995 C;Accession: S68993; S51132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Hilgarth, C.; Sauer, N.; Tanner, W.
J. Biol. Chem. 266, 24044-24047, 1991
A;Title: Glucose increases the expression of the ATP/ADP translocator and the glyceralde A;Reference number: A41677, MUID:92084708; PMID:1748677
A;Accession: A41677
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J. Biochem. 228, 86-91, 1
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183;
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                         Similarity
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                                                                                                 ADP, ATP carrier protein repeat ADP, ATP carrier protein repeat
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  Score 943; DB 2;
Pred. No. 7.6e-76;
5; Mismatches 62;
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Pred. No. 7.1e-79;
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                                                                                                                                                                                                                                                                                                                                                      ADP/ATP-transporter
PMID:7883016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Plasmodium falciparum)
                                                                                                    homology <ACP3:
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Search completed: December 18, 2003, 12:44:05 Job time : 15.3494 secs	RKGKEBIQYKNTIDCWIKILRNEGFKGFFKGAWANVIRGAGGALVLVFYDELQKLI 301	RKG-ADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGWGGAFVLVLYDELKKVI 298	186 IVYRGSYFGLYDSAKALLFTNDKNTNIVLKWAVAQSVTILAGLISYPFDTVRRRMMMMSG 245	185 IIYRAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQSG	127 AISLLIVYPLDFARTRLASDIGK-GKDRQFTGLFDCLAKIYKQTGLLSLYSGFGVSVTGI 185	125 ATSLCEVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGI 184	QGVLSLWRGNVANVIRYFPTQAFNFAFKDYFKNIF-PRYDQNTDFSKFFCVNILSGATAG 126	65 QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG 124	NFAADFLMGGISAAISKTVVTPIERVKMLIQTQDSIPBIKSGQVERYSGLINCFKRVSKE 67
	TRGAGGALVLVFYDBLQKLI 301	TRGMGGAFVLVLYDELKKVI 298	VTILAGLISYPPDTVRRRMMMSG	VTAVAGVVSYPFDTVRRRMMMQSG	LAKIYKQTGLLSLYSGFGVSVTGI	LVKITKSDGIRGLYQGFSVSVQGI	PRYDONTDESKEFCVNILSGATAG	GGVDKHTQFWRYFAGNLASGGAAG	PEIKSGQVERYSGLINCFKRVSKE
			245	243	185	184	126	124	67

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Database :
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length DB	B	Ħ	Description
ь	1474	95.5	298	13	Q8AYM3	Q8aym3 gallus gall
N	1451	94.0	298	ტ	Q8SQH5	Q8sqh5 bos taurus
w	1446	93.7	298		Q8JHI0	Q8jhi0 brachydanio
4	1422	92.2	298	σ	046373	046373 oryctolagus
ъ	1421	92.1	298	13	Q919M9	Q9i9m9 xenopus lae
σ	1414	91.6	298	片	Q8BVI9	
7	1409	91.3	298	13	Q9PRH1	_
æ	1406	91.1	298	13	Q9PRH2	? rana
9	1402	90.9	298	13	Q9YIC4	Q9yic4 rana rugosa
10	1300	84.3	299	ຫ	Q95VX4	ethmo
11	1259	81.6	317	13	Q91336	Q91336 rana sylvat
12	1254.5	81.3	312	ψı	Q8IRA0	
13	1235.5	80.1	. 300	ហ	Q9NHW5	
14	1187.5	77.0	288	ហ	044093	O44093 drogophila
15	1183.5	76.7	288	ψı	044094	
	1176 5	3				

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
749	753	756.5	759	760	764	767.5	778.5	827	924	924	932	936	943	944	944	946.5	947	973.5	993	993.5	996	1036.5	1038	1039	1041	1119	1137.5	1159
48.5	48.8	49.0	49.2	49.3	49.5	49.7	50.5	53.6	59.9	59.9	60.4	60.7	61.1	61.2	61.2	61.3	61.4	63.1	64.4	64.4	64.5	67.2	67.3	67.3	67.5	72.5	73.7	75.1
315	307	306	303	307	326	302	305	170	308	306	308	305	301	301	301	307	301	318	300	300	309	310	300	313	313	315	307	254
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Q8j0u1 gaeumannomy	Q26697 trypanosoma	Q18683 caenorhabdi	074260 candida par	076286 trypanosoma			Q9p8ml yarrowia li	Q9xs69 sus scrofa	Q8mvr6 nyctotherus	Q8mvr5 nyctotherus	_	Q8mvr7 nyctotherus	Q26006 plasmodium		Q25692 plasmodium				Q17407 caenorhabdi	001813 caenorhabdi	O97470 dictyosteli	Q8h727 phytophthor	O45865 caenorhabdi	P91410 caenorhabdi	Q21103 caenorhabdi	Q9h0c2 homo sapien	O62526 drosophila	Q8bkq5 mus musculu

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/ 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180	61 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120	/ 1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60	Query Match 95.5%; Score 1474; DB 13; Length 298; Best Local Similarity 93.0%; Pred. No. 2.5e-125; Matches 277; Conservative 14; Mismatches 7; Indels 0; Gaps 0;) . SEQUENCE 298 AA; 32847 MW; 1174CC5EC400A10D CRC64;	EMBL	FEBS Lett. 0:0-0(2002).	and ANT mRNA in chicken skeletal muscle.";	"Cold-induced mitochondrial uncoupling and expression of	A Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.;	SECURIORS	0 [1] - 1071 1071 1071 1			Eukaryota; Metazoa; Chordata;	Gallus gallus (Chicken).	AVANT.	ATP/ADP antiporter.	01-MAR-2003 (TrEMBLrel. 23, Last annotation	01-MAR-2003 (TrEMBLrel. 23,			O Q8AYM3 PRELIMINARY; PRT; 298 AA.	RESULT 1

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RESULT
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Q8SQH5;
01-JUN-2002
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                                                                                                                                               Q8JHI0;
01-OCT-2002
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                                              Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
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                 Eukaryota; Metazoa; Chordata
Actinopterygii; Neopterygii;
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Yamazaki N., Shinohara Y., Tanida K., Terada H.;

Yamazaki N., Shinohara Y., Tanida K., Terada H.;

"Structural properties of mammalian mitochondrial ADP/ATP carrie:
identification of possible amino acids that determine functional
differences in its isoforms.";

Mitochondrion 1:371-379 (2002).

EMBL; AB065433; BAB84673.1; -.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Boyinae; Bos
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Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
SEQUENCE 298 AA; 32955 MW; CB689
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                                                                                                                     22, Last sequence update)
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member 5 protein.
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                       Vertebrata; Euteleostomi;
Ostariophysi; Cypriniform
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                       Cypriniformes;
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Best Local Similarity
Matches 274; Conser
         J. Biochem. 335:541-547(1998).

-!- SIMILARITY: BELONGS TO THE MITOCHO
EMBL, AB09386; BAA2377.1;

InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
Pfam; PF00153; mito_carr; 3.

PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001993; Mitcoh_carrier.
InterPro; IPR002667; Mit_carrier.
InterPro; IPR002030; Mit_carrier.
InterPro; IPR0020301; Mit_uncoupling.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH CARRIER; 3.
SEQUENCE 298 AA; 32763 MW; D78663C
                                                                                                                                                                                                                                                                       O46373 PRELIMINARY;
O46373;
O1-JUN-1998 (TrEMBLrel. 0
O1-JUN-1998 (TrEMBLrel. 0
O1-MAR-2003 (TrEMBLrel. 2
ADP/ATP translocase.
                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolac
                                                                                                                       regulates calcium release from skeletal muscle.";
                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE-Skeletal mu
                                                                                                                                                                                                                NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Insertional mutagenesis in zebrafish rapidly identifies essential for early vertebrate development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Golling G., Amsterdam A., Sun Z., Antonelli
Burgess S., Haldi M., Artzt K., Farrington
Hopkins N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=22035902; PubMed=12006978;
Golling G., Amsterdam A., Sun Z.,
                                                                                                                                                  Yamaguchi N., Kasai M.;
"Identification of a 30kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nat. Genet. 31:135-140(2002)
EMBL; AF506216; AAM34660.1;
 PRINTS; PR00784; MTUNCOUPLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7955;
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                                                                                                                                                                              muscle;
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91.9%;
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Last sequence update)
Last annotation update)
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Pred. No. 8.5e-123;
L5; Mismatches 9;
                                                                                               MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D78663CF65C51D39 CRC64;
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                                                                                                                                                                                                                                                                                            A Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.;

T "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific a
T Dynamic Patterns of Expression During Development.";

L Submitted (FEB-2000) to the RMBI/GenBank/DDBJ databases.

C -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

R EMBL; APE31347; AAF63471.1; -.

R InterPro; IPR001993; Mitoch_Carrier.

InterPro; IPR001993; Mitoch_Carrier.

InterPro; IPR002067; Mit_uncoupling.

Pfam; PF00153; mito carri 3.

R Pfam; PF00153; mito carri 3.

R PRINTS; PR00926; MITOCH_CARRIER.

PRINTS; PR00926; MITOCH_CARRIER; 3.

Membrane; Transmembrane; Transport.

O SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;
                                                                                                                                                                                                    Matches
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Best L
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ANT1.
Xenopus laevis (African clawed frog).
Xenys laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Anura; Mesobatrachia; Pipoidea; Pipidae;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Venonodinae; Xenopus.
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01-OCT-2000
01-MAR-2003
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                               IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                               MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                               Score 1421; DB 13;
Pred. No. 1.6e-120;
4; Mismatches 15;
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Pred. No. 1.3e-120;
0; Mismatches 13;
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                                                                                         O9PRH1 PRELIMINARY;
O9PRH1;
O1-MAY-2000 (TrEMBLrel. 13,
O1-MAY-2000 (TrEMBLrel. 13,
O1-MAR-2003 (TrEMBLrel. 23,
ADP/ATP translocase.
Rana rugosa (Wrinkled frog).
Bukaryota, Metazoa, Chordata,
Amphibia, Batrachia, Anura, Ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Medulla ob
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
Solute carrier family 25.
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Q9PRH2;
01-MAY-2000
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01-MAY-2000 (TrEMBLrel.
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ADP/ATP translocase.
                                                                                                                                                    MEDLINE=99083429; PubMed=9866197; Miura I., Ohtani H., Nakamura M.,
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_nncoupling.
Pfam; PP00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00794; MITOCARRIER.
PRINTS; PR007184; MITOCH_CARRIER; 3.
Membrane; Transmembrane; Transport.
SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;
                                           Pfam; PF00153; mito carr; 3.

PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Membrane; Transmembrane; Transport.
SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;
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01-MAY-1999 (TREMBLIEGL 10,
01-MAR-2003 (TREMBLIEGL 23,
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
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EMBL; AP401758; AAL02100.1; -.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PF10153; mito_carr; 3.
PROSITE; PR00926; MITOCH_CARRIER; 3.
SEQUENCE 299 AA; 33037 MW; 3C3BBCB26E7C3C5E CRC64;
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"Nucleotide sequence
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Pleurostigmophora; Scolopendromorpha; Scolopendridae;
NCBI_TaxID=62613;
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Cai Q., Storey K.B.;

L. Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

L. Submitted (APR-1999) to the MITOCHONDRIAL CARRIER FAMI.

C. -- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMI.

R. EMBL; U44832; AAA97882.2; --

R. InterPro; IPR001993; Mitoch carrier.

R. InterPro; IPR002067; Mit_carrier.

R. PFAMM; PPF00153; mito carr; 3.

R. PRINTS; PR00926; MITOCHARRIER.

R. PROSITE; PS00215; MITOCH_CARRIER; 3.

Membrane; Transmembrane; Transport.

W. Membrane; Transmembrane; Transport.

G. SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72 CRC64;
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Best Local Similarity
Matches 236; Conserv
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hrasapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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Cai Q., Greenway S.C., Storey K.B.;
"Differential regulation of the mitochondrial
in wood frogs under freezing stress.";
Biochim. Biophys. Acta 1353:69-78(1997).
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01-NOV-1996 (TrEMBLrel. 01,
01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2003 (TrEMBLrel. 23,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
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Pred. No. 8
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Mamban M.D. Collière S. B. Holt R.M., Forans C.A., Godayne J.D.,
RA Ammantides P.G., Scherrer S.E., Lik P.M., Forans C.A., Golave J.D.,
RA Ammantides P.G., Scherrer S.E., Lik P.M., Forans C.A., Golave P.F.,
RA George R.A., Lewis S.E., Richards S., Amburar M., Henderson S.M.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Feiffer B.D.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Santhon R.C., Rogers Y.H., Blaars R.G., Change M., Feiffer B.D.,
RA Man K.H. P. Doy, G. P. Barter B.G., Change M., Feiffer B.D.,
RA Man K.H. P. Doy, G. P. Barter B.G., Change M., Feiffer B.D.,
RA Man K.H. P. Doy, G. P. Barter B.G., Change M., Feiffer B.D.,
RA Buttis K.C., Busam D.A., Butlet H., Gadleu B., Center A., Chadrad I.,
RA Buttis K.C., Busam D.A., Butlet H., Cadleu B., Center A., Chadrad I.,
RA Buttis K.C., Busam D.A., Butlet H., Cadleu B., Center A., Chadrad I.,
RA Goldek A., Goog F., Gorrell J.H., Oz., Golbert M., Merker B.M.,
RA Goldek A., Goog F., Gorrell J.H., Gu. J., Golbert M., Merker B.M.,
RA Harris N.L., Harvey D., Helman T.J., Hermandes J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hermandes J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Well M.H., Degwan D.L.,
RA Harris N.L., May M., Murphy B., Murphy L., Murphy D.M., Nalom D.L.,
RA Harris N.L., May M., Murphy B., Murphy L., Murphy L., Murphy L.,
RA Harris N.L., Rannington K., Standers R.D., Scheet R.P., Brotheld J.M.,
RA Harris N.L., Harvey D., Helman T.J., Hermandes J.R., Houck J.,
RA Harris N.L., May M., Murphy B., Murphy L., Murphy L., Murphy J.M., Nalom D.L.,
RA Harris N.L., Rannington K., Standers R.D., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Scheet R.P., Schee
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Matches 233
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Best Local Similarity
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Membrane;
SEQUENCE
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Lucilla cuprina (Greenbottle fly) (Australian sheep blowfly).
Lucilla cuprina (Greenbottle fly) (Australian sheep blowfly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
Calliphoridae; Lucilia.
NCBI_TaxID=7375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AE003484; AAN09267.1; -
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PROSITE; PS00215; MITOCH CARRIER; 3.
Membrane; Transmembrane; Transport.
SEQUENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=SS mal
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                                                                                           IIYRAAYFGVYDTAKGMLPDFKNTHIVVSWMIAQTVTAVAGVVSYFFDTVRRRMMQSGR
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Conservative
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                                                                                                                                                                                                                                                                                      80.1%; Score 1235.5;
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Last annotation update)
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23; Mismatches
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RESULT 15
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EMBL; AF025798; AAB87883.1; --
FlyBase; FBgn0023292; Dpse\sesB.
InterPro; IFR001993; Mitoch_carrier.
InterPro; IFR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCH_CARRIER.
PROSITE; PR00926; MITOCH_CARRIER; 3.
Membrane; Repeat; Transmembrane; Transport.
NON_TER
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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PRINTS; PR00926; MITOCARRIER.
PROSITS; PS00215; MITOCH CARRIER; 3.
Membrane; Repeat; Transmembrane; Transport.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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KATEIIYKNTIHCWGTIAKQE-GTAFFKGAFSNVLRGTGGAFVLV
                                             KGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLV
                                                                                                                         IIYRAAYFGFYDTAR-MLPDPKNTPIYISWAIAQCVTTVAGIVSYPPDTVRRRMMQSGR
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31775 MW; 06A1D1B477B81B26 CRC64;
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